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(54) Title: NON-ENDOGENOUS, CONSTITUTIVELY ACTIVATED HUMAN G PROTEIN-COUPLED RECEPTORS		
(57) Abstract <p>Disclosed herein are constitutively activated, non-endogenous versions of endogenous human G protein-coupled receptors comprising (a) the following amino acid sequence region (C-terminus to N-terminus orientation) and/or (b) the following nucleic acid sequence region (3' to 5' orientation) transverse the transmembrane-6 (TM6) and intracellular loop-3 (IC3) regions of the GPCR: (a) P¹ AA₁₅ X and/or (b) P^{codon} (AA-codon)₁₅ X_{codon}, respectively. In a most preferred embodiment, P¹ and P^{codon} are endogenous proline and an endogenous nucleic acid encoding region encoding proline, respectively, located within TM6 of the non-endogenous GPCR; AA₁₅ and (AA-codon)₁₅ are 15 endogenous amino acid residues and 15 codons encoding endogenous amino acid residues, respectively; and X and X_{codon} are non-endogenous lysine and a non-endogenous nucleic acid encoding region encoding lysine, respectively, located within IC3 of the non-endogenous GPCR. Because it is most preferred that the non-endogenous human GPCRs which incorporate these mutations are incorporated into mammalian cells and utilized for the screening of the candidate compounds, the non-endogenous human GPCR incorporating the mutation need not be purified and isolated <i>per se</i> (i.e., these are incorporated within the cellular membrane of a mammalian cell), although such purified and isolated non-endogenous human GPCRs are well within the purview of this disclosure.</p>		

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**NON-ENDOGENOUS, CONSTITUTIVELY ACTIVATED
HUMAN G PROTEIN-COUPLED RECEPTORS**

The benefits of commonly owned U.S. Serial Number 09/170,496, filed October 13, 1998, U.S. Serial Number 08/839, 449 filed April 14, 1997 (now abandoned),
5 U.S. Serial Number 09/060,188, filed April 14, 1998; U.S. Provisional Number 60/090,783, filed June 26, 1998; and U.S. Provisional Number 60/095,677, filed on August 7, 1998, are hereby claimed. Each of the foregoing applications are incorporated by reference herein in their entirety.

FIELD OF THE INVENTION

10 The invention disclosed in this patent document relates to transmembrane receptors, and more particularly to human G protein-coupled receptors (GPCRs) which have been altered such that altered GPCRs are constitutively activated. Most preferably, the altered human GPCRs are used for the screening of therapeutic compounds.

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BACKGROUND OF THE INVENTION

Although a number of receptor classes exist in humans, by far the most abundant and therapeutically relevant is represented by the G protein-coupled receptor (GPCR or GPCRs) class. It is estimated that there are some 100,000 genes within the human genome, and of these, approximately 2% or 2,000 genes, are estimated to code for GPCRs. Of these, there are approximately 100 GPCRs for which the endogenous ligand that binds to the GPCR has been identified. Because of the significant time-lag that exists between the discovery of an endogenous GPCR and its endogenous ligand, it can be presumed that the remaining 1,900 GPCRs will be identified and characterized long before the endogenous ligands for these receptors are identified. Indeed, the rapidity by which the Human Genome Project is sequencing the 100,000 human genes indicates that the remaining human GPCRs will be fully sequenced within the next few years. Nevertheless, and despite the efforts to sequence the human genome, it is still very unclear as to how scientists will be able to rapidly, effectively and efficiently exploit this information to improve and enhance the human condition. The present invention is geared towards this important objective.

Receptors, including GPCRs, for which the endogenous ligand has been identified are referred to as "known" receptors, while receptors for which the endogenous ligand has not been identified are referred to as "orphan" receptors. This distinction is not merely semantic, particularly in the case of GPCRs. GPCRs represent an important area for the development of pharmaceutical products: from approximately 20 of the 100 known GPCRs, 60% of all prescription pharmaceuticals have been developed. Thus, the orphan GPCRs are to the pharmaceutical industry what gold was to California in the late 19th century - an opportunity to drive growth, expansion, enhancement and development. A serious drawback exists, however,

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with orphan receptors relative to the discovery of novel therapeutics. This is because the traditional approach to the discovery and development of pharmaceuticals has required access to both the receptor *and* its endogenous ligand. Thus, heretofore, orphan GPCRs have presented the art with a tantalizing and undeveloped resource for the discovery of pharmaceuticals.

- 5 Under the traditional approach to the discovery of potential therapeutics, it is generally the case that the receptor is first identified. Before drug discovery efforts can be initiated, elaborate, time consuming and expensive procedures are typically put into place in order to identify, isolate and generate the receptor's endogenous ligand - this process can require from between 3 and ten years per receptor, at a cost of about \$5million (U.S.) per receptor. These time and financial
- 10 resources must be expended before the traditional approach to drug discovery can commence. This is because traditional drug discovery techniques rely upon so-called "competitive binding assays" whereby putative therapeutic agents are "screened" against the receptor in an effort to discover compounds that either block the endogenous ligand from binding to the receptor ("antagonists"), or enhance or mimic the effects of the ligand binding to the receptor ("agonists").
- 15 The overall objective is to identify compounds that prevent cellular activation when the ligand binds to the receptor (the antagonists), or that enhance or increase cellular activity that would otherwise occur if the ligand was properly binding with the receptor (the agonists). Because the endogenous ligands for orphan GPCRs are by definition not identified, the ability to discover novel and unique therapeutics to these receptors using traditional drug discovery techniques is not
- 20 possible. The present invention, as will be set forth in greater detail below, overcomes these and other severe limitations created by such traditional drug discovery techniques.

GPCRs share a common structural motif. All these receptors have seven sequences of between 22 to 24 hydrophobic amino acids that form seven alpha helices, each of which spans the

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membrane (each span is identified by number, *i.e.*, transmembrane-1 (TM-1), transmembrane-2 (TM-2), etc.). The transmembrane helices are joined by strands of amino acids between transmembrane-2 and transmembrane-3, transmembrane-4 and transmembrane-5, and transmembrane-6 and transmembrane-7 on the exterior, or "extracellular" side, of the cell membrane (these are referred to as "extracellular" regions 1, 2 and 3 (EC-1, EC-2 and EC-3), respectively). The transmembrane helices are also joined by strands of amino acids between transmembrane-1 and transmembrane-2, transmembrane-3 and transmembrane-4, and transmembrane-5 and transmembrane-6 on the interior, or "intracellular" side, of the cell membrane (these are referred to as "intracellular" regions 1, 2 and 3 (IC-1, IC-2 and IC-3), respectively). The "carboxy" ("C") terminus of the receptor lies in the intracellular space within the cell, and the "amino" ("N") terminus of the receptor lies in the extracellular space outside of the cell. The general structure of G protein-coupled receptors is depicted in Figure 1.

Generally, when an endogenous ligand binds with the receptor (often referred to as "activation" of the receptor), there is a change in the conformation of the intracellular region that allows for coupling between the intracellular region and an intracellular "G-protein." Although other G proteins exist, currently, Gq, Gs, Gi, and Go are G proteins that have been identified. Endogenous ligand-activated GPCR coupling with the G-protein begins a signaling cascade process (referred to as "signal transduction"). Under normal conditions, signal transduction ultimately results in cellular activation or cellular inhibition. It is thought that the IC-3 loop as well as the carboxy terminus of the receptor interact with the G protein. A principal focus of this invention is directed to the transmembrane-6 (TM6) region and the intracellular-3 (IC3) region of the GPCR.

Under physiological conditions, GPCRs exist in the cell membrane in equilibrium between

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two different conformations: an "inactive" state and an "active" state. As shown schematically in Figure 2, a receptor in an inactive state is unable to link to the intracellular signaling transduction pathway to produce a biological response. Changing the receptor conformation to the active state allows linkage to the transduction pathway (via the G-protein) and produces a biological response.

5 A receptor may be stabilized in an active state by an endogenous ligand or a compound such as a drug. Recent discoveries, including but not exclusively limited to modifications to the amino acid sequence of the receptor, provide means other than endogenous ligands or drugs to promote and stabilize the receptor in the active state conformation. These means effectively stabilize the receptor in an active state by simulating the effect of an endogenous ligand binding
10 to the receptor. Stabilization by such ligand-independent means is termed "constitutive receptor activation."

As noted above, the use of an orphan receptor for screening purposes has not been possible. This is because the traditional "dogma" regarding screening of compounds mandates that the ligand for the receptor be known. By definition, then, this approach has no applicability with
15 respect to orphan receptors. Thus, by adhering to this dogmatic approach to the discovery of therapeutics, the art, in essence, has taught and has been taught to forsake the use of orphan receptors unless and until the endogenous ligand for the receptor is discovered. Given that there are an estimated 2,000 G protein coupled receptors, the majority of which are orphan receptors, such dogma castigates a creative, unique and distinct approach to the discovery of therapeutics.

20 Information regarding the nucleic acid and/or amino acid sequences of a variety of GPCRs is summarized below in Table A. Because an important focus of the invention disclosed herein is directed towards orphan GPCRs, many of the below-cited references are related to orphan GPCRs. However, this list is not intended to imply, nor is this list to be construed, legally or

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otherwise, that the invention disclosed herein is only applicable to orphan GPCRs or the specific GPCRs listed below. Additionally, certain receptors that have been isolated are not the subject of publications per se; for example, reference is made to a G Protein-Coupled Receptor database on the "world-wide web" (neither the named inventors nor the assignee have any affiliation with this site) that lists GPCRs. Other GPCRs are the subject of patent applications owned by the present assignee and these are not listed below (including GPR3, GPR6 and GPR12; see U.S. Provisional Number 60/094879):

Table A

Receptor Name	Publication Reference
GPR1	23 Genomics 609 (1994)
GPR4	14 DNA and Cell Biology 25 (1995)
GPR5	14 DNA and Cell Biology 25 (1995)
GPR7	28 Genomics 84 (1995)
GPR8	28 Genomics 84 (1995)
GPR9	184 J. Exp. Med. 963 (1996)
GPR10	29 Genomics 335 (1995)
GPR15	32 Genomics 462 (1996)
GPR17	70 J Neurochem. 1357 (1998)
GPR18	42 Genomics 462 (1997)
GPR20	187 Gene 75 (1997)
GPR21	187 Gene 75 (1997)
GPR22	187 Gene 75 (1997)
GPR24	398 FEBS Lett. 253 (1996)
GPR30	45 Genomics 607 (1997)
GPR31	42 Genomics 519 (1997)
GPR32	50 Genomics 281 (1997)
GPR40	239 Biochem. Biophys. Res. Commun. 543 (1997)
GPR41	239 Biochem. Biophys. Res. Commun. 543 (1997)
GPR43	239 Biochem. Biophys. Res. Commun. 543 (1997)
APJ	136 Gene 355 (1993)
BLR1	22 Eur. J. Immunol. 2759 (1992)
CEPR	231 Biochem. Biophys. Res. Commun. 651 (1997)
EBI1	23 Genomics 643 (1994)
EBI2	67 J. Virol. 2209 (1993)
ETBR-LP2	424 FEBS Lett. 193 (1998)
GPCR-CNS	54 Brain Res. Mol. Brain Res. 152 (1998); 45 Genomics 68 (1997)
GPR-NGA	394 FEBS Lett. 325 (1996)
H9	386 FEBS Lett 219 (1996)

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HBA954	1261 Biochim. Biophys. Acta 121 (1995)
HG38	247 Biochem. Biophys. Res. Commun. 266 (1998)
HM74	5 Int. Immunol. 1239 (1993)
OGR1	35 Genomics 397 (1996)
V28	163 Gene 295 (1995)

5

As will be set forth and disclosed in greater detail below, utilization of a mutational cassette to modify the endogenous sequence of a human GPCR leads to a constitutively activated version of the human GPCR. These non-endogenous, constitutively activated versions of human GPCRs can be utilized, *inter alia*, for the screening of candidate compounds to directly identify compounds

10 of, *e.g.*, therapeutic relevance.

SUMMARY OF THE INVENTION

Disclosed herein is a non-endogenous, human G protein-coupled receptor comprising (a) as a most preferred amino acid sequence region (C-terminus to N-terminus orientation) and/or (b) as a most preferred nucleic acid sequence region (3' to 5' orientation) transversing the transmembrane-6 (TM6) and intracellular loop-3 (IC3) regions of the GPCR:

15 the transmembrane-6 (TM6) and intracellular loop-3 (IC3) regions of the GPCR:

(a) P¹ AA₁₅ X

wherein:

- (1) P¹ is an amino acid residue located within the TM6 region of the GPCR, where P¹ is selected from the group consisting of (i) the endogenous GPCR's proline residue, and (ii) a non-endogenous amino acid residue other than proline;
- (2) AA₁₅ are 15 amino acids selected from the group consisting of

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(a) the endogenous GPCR's amino acids (b) non-endogenous amino acid residues, and (c) a combination of the endogenous GPCR's amino acids and non-endogenous amino acids, excepting that none of the 15 endogenous amino acid residues that are positioned within the TM6 region of the GPCR is proline; and

(3) X is a non-endogenous amino acid residue located within the IC3 region of said GPCR, preferably selected from the group consisting of lysine, histidine and arginine, and most preferably lysine, excepting that when the endogenous amino acid at position X is lysine, then X is an amino acid other than lysine, preferably alanine;

and/or

(b) P^{codon} (AA-codon)₁₅ X_{codon}

15 wherein:

- (1) P^{codon} is a nucleic acid sequence within the TM6 region of the GPCR, where P^{codon} encodes an amino acid selected from the group consisting of (i) the endogenous GPCR's proline residue, and (ii) a non-endogenous amino acid residue other than proline;
- (2) (AA-codon)₁₅ are 15 codons encoding 15 amino acids selected from the group consisting of (a) the endogenous GPCR's amino acids (b) non-endogenous amino acid residues and (c) a combination of the endogenous GPCR's amino acids and non-

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endogenous amino acids, excepting that none of the 15 endogenous codons within the TM6 region of the GPCR encodes a proline amino acid residue; and

- (3) X_{codon} is a nucleic acid encoding region residue located within the IC3 region of said GPCR, where X_{codon} encodes a non-endogenous amino acid, preferably selected from the group consisting of lysine, histidine and arginine, and most preferably lysine, excepting that when the endogenous encoding region at position X_{codon} encodes the amino acid lysine, then X_{codon} encodes an amino acid other than lysine, preferably alanine.

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The terms endogenous and non-endogenous in reference to these sequence cassettes are relative to the endogenous GPCR. For example, once the endogenous proline residue is located within the TM6 region of a particular GPCR, and the 16th amino acid therefrom is identified for mutation to constitutively activate the receptor, it is also possible to mutate the endogenous proline residue (i.e., once the marker is located and the 16th amino acid to be mutated is identified, one may mutate the marker itself), although it is most preferred that the proline residue not be mutated. Similarly, and while it is most preferred that AA₁₅ be maintained in their endogenous forms, these amino acids may also be mutated. The only amino acid that must be mutated in the non-endogenous version of the human GPCR is X i.e., the endogenous amino acid that is 16 residues from P¹ cannot be maintained in its endogenous form and must be mutated, as further disclosed herein. Stated again, while it is preferred that in the non-endogenous version of the human GPCR, P¹ and AA₁₅ remain in their endogenous forms (i.e., identical to their wild-type forms), once X is identified and mutated, any and/or all of P¹ and AA₁₅ can be mutated. This applies to the nucleic

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acid sequences as well. In those cases where the endogenous amino acid at position X is lysine, then in the non-endogenous version of such GPCR, X is an amino acid other than lysine, preferably alanine.

Accordingly, and as a hypothetical example, if the endogenous GPCR has the following
5 endogenous amino acid sequence at the above-noted positions:

P-AACCTTGRRRDDDE -Q

then any of the following exemplary and hypothetical cassettes would fall within the scope of the disclosure (non-endogenous amino acids are set forth in bold):

P-AACCTTGRRRDDDE -K

10 P-AACCT**TH**IGRRRDDDE -K

P-ADEETTGRRRDDDE -A

P-LLKFMSTWZLVAA**PQ** -K

A-LLKFMSTWZLVAA**PQ** -K

It is also possible to add amino acid residues within AA₁₅, but such an approach is not particularly
15 advanced. Indeed, in the most preferred embodiments, the only amino acid that differs in the non-endogenous version of the human GPCR as compared with the endogenous version of that GPCR is the amino acid in position X; mutation of this amino acid itself leads to constitutive activation of the receptor.

Thus, in particularly preferred embodiments, P¹ and P^{codon} are endogenous proline and an
20 endogenous nucleic acid encoding region encoding proline, respectively; and X and X_{codon} are non-endogenous lysine or alanine and a non-endogenous nucleic acid encoding region encoding lysine or alanine, respectively, with lysine being most preferred. Because it is most preferred that the non-endogenous versions of the human GPCRs which incorporate these mutations are

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incorporated into mammalian cells and utilized for the screening of candidate compounds, the non-endogenous human GPCR incorporating the mutation need not be purified and isolated *per se* (i.e., these are incorporated within the cellular membrane of a mammalian cell), although such purified and isolated non-endogenous human GPCRs are well within the purview of this disclosure. Gene-targeted and transgenic non-human mammals (preferably rats and mice) incorporating the non-endogenous human GPCRs are also within the purview of this invention; in particular, gene-targeted mammals are most preferred in that these animals will incorporate the non-endogenous versions of the human GPCRs in place of the non-human mammal's endogenous GPCR-encoding region (techniques for generating such non-human mammals to replace the non-human mammal's protein encoding region with a human encoding region are well known; see, for example, U.S. Patent No. 5,777,194.)

It has been discovered that these changes to an endogenous human GPCR render the GPCR constitutively active such that, as will be further disclosed herein, the non-endogenous, constitutively activated version of the human GPCR can be utilized for, *inter alia*, the direct screening of candidate compounds without the need for the endogenous ligand. Thus, methods for using these materials, and products identified by these methods are also within the purview of the following disclosure.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows a generalized structure of a G protein-coupled receptor with the numbers assigned to the transmembrane helices, the intracellular loops, and the extracellular loops.

Figure 2 schematically shows the two states, active and inactive, for a typical G protein coupled receptor and the linkage of the active state to the second messenger transduction pathway.

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Figure 3 is a sequence diagram of the preferred vector pCMV, including restriction enzymen site locations.

Figure 4 is a diagrammatic representation of the signal measured comparing pCMV, non-endogenous, constitutively active GPR30 inhibition of GPR6-mediated activation of CRE-Luc
5 reporter with endogenous GPR30 inhibition of GPR6-mediated activation of CRE-Luc reporter.

Figure 5 is a diagrammatic representation of the signal measured comparing pCMV, non-endogenous, constitutively activated GPR17 inhibition of GPR3-mediated activation of CRE-Luc
10 reporter with endogenous GPR17 inhibition of GPR3-mediated activation of CRE-Luc reporter.

Figure 6 provides diagrammatic results of the signal measured comparing control pCMV, endogenous APJ and non-endogenous APJ.

Figure 7 provides an illustration of IP₃ production from non-endogenous human 5-HT_{2A} receptor as compared to the endogenous version of this receptor.

15 Figure 8 are dot-blot format results for GPR1 (8A), GPR30 (8B) and APJ (8C).

DETAILED DESCRIPTION

The scientific literature that has evolved around receptors has adopted a number of terms to refer to ligands having various effects on receptors. For clarity and consistency, the following definitions will be used throughout this patent document. To the extent that these definitions
20 conflict with other definitions for these terms, the following definitions shall control:

AGONISTS shall mean compounds that activate the intracellular response when they bind to the receptor, or enhance GTP binding to membranes.

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AMINO ACID ABBREVIATIONS used herein are set below:

	ALANINE	ALA	A
	ARGININE	ARG	R
	ASPARAGINE	ASN	N
5	ASPARTIC ACID	ASP	D
	CYSTEINE	CYS	C
	GLUTAMIC ACID	GLU	E
	GLUTAMINE	GLN	Q
	GLYCINE	GLY	G
10	HISTIDINE	HIS	H
	ISOLEUCINE	ILE	I
	LEUCINE	LEU	L
	LYSINE	LYS	K
	METHIONINE	MET	M
15	PHENYLALANINE	PHE	F
	PROLINE	PRO	P
	SERINE	SER	S
	THREONINE	THR	T
	TRYPTOPHAN	TRP	W
20	TYROSINE	TYR	Y
	VALINE	VAL	V

PARTIAL AGONISTS shall mean compounds which activate the intracellular response when they bind to the receptor to a lesser degree/extent than do agonists, or enhance GTP binding to membranes to a lesser degree/extent than do agonists

25 **ANTAGONIST** shall mean compounds that competitively bind to the receptor at the same site as the agonists but which do not activate the intracellular response initiated by the active form of the receptor, and can thereby inhibit the intracellular responses by agonists or partial agonists. **ANTAGONISTS** do not diminish the baseline intracellular response in the absence of an agonist or partial agonist.

30 **CANDIDATE COMPOUND** shall mean a molecule (for example, and not limitation, a chemical compound) which is amenable to a screening technique. Preferably, the phrase

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"candidate compound" does not include compounds which were publicly known to be compounds selected from the group consisting of inverse agonist, agonist or antagonist to a receptor, as previously determined by an indirect identification process ("indirectly identified compound"); more preferably, not including an indirectly identified compound which has previously been
5 determined to have therapeutic efficacy in at least one mammal; and, most preferably, not including an indirectly identified compound which has previously been determined to have therapeutic utility in humans.

CODON shall mean a grouping of three nucleotides (or equivalents to nucleotides) which generally comprise a nucleoside (adenosine (A), guanosine (G), cytidine (C), uridine (U) and
10 thymidine (T)) coupled to a phosphate group and which, when translated, encodes an amino acid.

COMPOUND EFFICACY shall mean a measurement of the ability of a compound to inhibit or stimulate receptor functionality, as opposed to receptor binding affinity. A preferred means of detecting compound efficacy is via measurement of, *e.g.*, [³⁵S]GTPγS binding, as further disclosed in the Example section of this patent document.

15 **CONSTITUTIVELY ACTIVATED RECEPTOR** shall mean a receptor subject to constitutive receptor activation. In accordance with the invention disclosed herein, a non-endogenous, human constitutively activated G protein-coupled receptor is one that has been mutated to include the amino acid cassette P¹AA₁₅X, as set forth in greater detail below.

CONSTITUTIVE RECEPTOR ACTIVATION shall mean stabilization of a receptor
20 in the active state by means other than binding of the receptor with its endogenous ligand or a chemical equivalent thereof. Preferably, a G protein-coupled receptor subjected to constitutive receptor activation in accordance with the invention disclosed herein evidences at least a 10% difference in response (increase or decrease, as the case may be) to the signal measured for

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constitutive activation as compared with the endogenous form of that GPCR, more preferably, about a 25% difference in such comparative response, and most preferably about a 50% difference in such comparative response. When used for the purposes of directly identifying candidate compounds, it is most preferred that the signal difference be at least about 50% such that there is

5 a sufficient difference between the endogenous signal and the non-endogenous signal to differentiate between selected candidate compounds. In most instances, the "difference" will be an increase in signal; however, with respect to Gs-coupled GPCRS, the "difference" measured is preferably a decrease, as will be set forth in greater detail below.

CONTACT or **CONTACTING** shall mean bringing at least two moieties together,

10 whether in an in vitro system or an in vivo system.

DIRECTLY IDENTIFYING or **DIRECTLY IDENTIFIED**, in relationship to the phrase "candidate compound", shall mean the screening of a candidate compound against a constitutively activated G protein-coupled receptor, and assessing the compound efficacy of such compound. This phrase is, under no circumstances, to be interpreted or understood to be

15 encompassed by or to encompass the phrase "indirectly identifying" or "indirectly identified."

ENDOGENOUS shall mean a material that is naturally produced by the genome of the species. **ENDOGENOUS** in reference to, for example and not limitation, GPCR, shall mean that which is naturally produced by a human, an insect, a plant, a bacterium, or a virus. By contrast, the term **NON-ENDOGENOUS** in this context shall mean that which is not naturally produced

20 by the genome of a species. For example, and not limitation, a receptor which is not constitutively active in its endogenous form, but when mutated by using the cassettes disclosed herein and thereafter becomes constitutively active, is most preferably referred to herein as a "non-endogenous, constitutively activated receptor." Both terms can be utilized to describe both "in

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vivo" and "in vitro" systems. For example, and not limitation, in a screening approach, the endogenous or non-endogenous receptor may be in reference to an in vitro screening system whereby the receptor is expressed on the cell-surface of a mammalian cell. As a further example and not limitation, where the genome of a mammal has been manipulated to include a non-
5 endogenous constitutively activated receptor, screening of a candidate compound by means of an in vivo system is viable.

HOST CELL shall mean a cell capable of having a Plasmid and/or Vector incorporated therein. In the case of a prokaryotic Host Cell, a Plasmid is typically replicated as an autonomous molecule as the Host Cell replicates (generally, the Plasmid is thereafter isolated for introduction
10 into a eukaryotic Host Cell); in the case of a eukaryotic Host Cell, a Plasmid is integrated into the cellular DNA of the Host Cell such that when the eukaryotic Host Cell replicates, the Plasmid replicates. Preferably, for the purposes of the invention disclosed herein, the Host Cell is eukaryotic, more preferably, mammalian, and most preferably selected from the group consisting of 293, 293T and COS-7 cells.

15 **INDIRECTLY IDENTIFYING** or **INDIRECTLY IDENTIFIED** means the traditional approach to the drug discovery process involving identification of an endogenous ligand specific for an endogenous receptor, screening of candidate compounds against the receptor for determination of those which interfere and/or compete with the ligand-receptor interaction, and assessing the efficacy of the compound for affecting at least one second messenger pathway
20 associated with the activated receptor.

INHIBIT or **INHIBITING**, in relationship to the term "response" shall mean that a response is decreased or prevented in the presence of a compound as opposed to in the absence of the compound.

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INVERSE AGONISTS shall mean compounds which bind to either the endogenous form of the receptor or to the constitutively activated form of the receptor, and which inhibit the baseline intracellular response initiated by the active form of the receptor below the normal base level of activity which is observed in the absence of agonists or partial agonists, or decrease GTP binding to membranes. Preferably, the baseline intracellular response is inhibited in the presence of the inverse agonist by at least 30%, more preferably by at least 50%, and most preferably by at least 75%, as compared with the baseline response in the absence of the inverse agonist.

KNOWN RECEPTOR shall mean an endogenous receptor for which the endogenous ligand specific for that receptor has been identified.

LIGAND shall mean an endogenous, naturally occurring molecule specific for an endogenous, naturally occurring receptor.

MUTANT or **MUTATION** in reference to an endogenous receptor's nucleic acid and/or amino acid sequence shall mean a specified change or changes to such endogenous sequences such that a mutated form of an endogenous, non-constitutively activated receptor evidences constitutive activation of the receptor. In terms of equivalents to specific sequences, a subsequent mutated form of a human receptor is considered to be equivalent to a first mutation of the human receptor if (a) the level of constitutive activation of the subsequent mutated form of the receptor is substantially the same as that evidenced by the first mutation of the receptor; and (b) the percent sequence (amino acid and/or nucleic acid) homology between the subsequent mutated form of the receptor and the first mutation of the receptor is at least about 80%, more preferably at least about 90% and most preferably at least 95%. Ideally, and owing to the fact that the most preferred cassettes disclosed herein for achieving constitutive activation includes a single amino acid and/or codon change between the endogenous and the non-endogenous forms of the GPCR (i.e. X or

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X_{codon}), the percent sequence homology should be at least 98%.

ORPHAN RECEPTOR shall mean an endogenous receptor for which the endogenous ligand specific for that receptor has not been identified or is not known.

PHARMACEUTICAL COMPOSITION shall mean a composition comprising at least
5 one active ingredient, whereby the composition is amenable to investigation for a specified, efficacious outcome in a mammal (for example, and not limitation, a human). Those of ordinary skill in the art will understand and appreciate the techniques appropriate for determining whether an active ingredient has a desired efficacious outcome based upon the needs of the artisan.

PLASMID shall mean the combination of a Vector and cDNA. Generally, a Plasmid is
10 introduced into a Host Cell for the purpose of replication and/or expression of the cDNA as a protein.

STIMULATE or **STIMULATING**, in relationship to the term "response" shall mean that a response is increased in the presence of a compound as opposed to in the absence of the compound.

15 **TRANSVERSE** or **TRANSVERSING**, in reference to either a defined nucleic acid sequence or a defined amino acid sequence, shall mean that the sequence is located within at least two different and defined regions. For example, in an amino acid sequence that is 10 amino acid moieties in length, where 3 of the 10 moieties are in the TM6 region of a GPCR and the remaining 7 moieties are in the IC3 region of the GPCR, the 10 amino acid moiety can be described as
20 transversing the TM6 and IC3 regions of the GPCR.

VECTOR in reference to cDNA shall mean a circular DNA capable of incorporating at least one cDNA and capable of incorporation into a Host Cell.

The order of the following sections is set forth for presentational efficiency and is not

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intended, nor should be construed, as a limitation on the disclosure or the claims to follow.

A. Introduction

The traditional study of receptors has always proceeded from the a priori assumption (historically based) that the endogenous ligand must first be identified before discovery could proceed to find antagonists and other molecules that could affect the receptor. Even in cases where an antagonist might have been known first, the search immediately extended to looking for the endogenous ligand. This mode of thinking has persisted in receptor research even after the discovery of constitutively activated receptors. What has not been heretofore recognized is that it is the active state of the receptor that is most useful for discovering agonists, partial agonists, and inverse agonists of the receptor. For those diseases which result from an overly active receptor or an under-active receptor, what is desired in a therapeutic drug is a compound which acts to diminish the active state of a receptor or enhance the activity of the receptor, respectively, not necessarily a drug which is an antagonist to the endogenous ligand. This is because a compound that reduces or enhances the activity of the active receptor state need not bind at the same site as the endogenous ligand. Thus, as taught by a method of this invention, any search for therapeutic compounds should start by screening compounds against the ligand-independent active state.

Screening candidate compounds against non-endogenous, constitutively activated GPCRs allows for the direct identification of candidate compounds which act at these cell surface receptors, without requiring any prior knowledge or use of the receptor's endogenous ligand. By determining areas within the body where the endogenous version of such GPCRs are expressed and/or over-expressed, it is possible to determine related disease/disorder states which are associated with the expression and/or over-expression of these receptors; such an approach is disclosed in this patent document.

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B. Disease/Disorder Identification and/or Selection

Most preferably, inverse agonists to the non-endogenous, constitutively activated GPCRs can be identified using the materials of this invention. Such inverse agonists are ideal candidates as lead compounds in drug discovery programs for treating diseases related to these receptors.

- 5 Because of the ability to directly identify inverse agonists, partial agonists or agonists to these receptors, thereby allowing for the development of pharmaceutical compositions, a search, for diseases and disorders associated with these receptors is possible. For example, scanning both diseased and normal tissue samples for the presence of these receptor now becomes more than an academic exercise or one which might be pursued along the path of identifying, in the case of an
- 10 orphan receptor, an endogenous ligand. Tissue scans can be conducted across a broad range of healthy and diseased tissues. Such tissue scans provide a preferred first step in associating a specific receptor with a disease and/or disorder.

Preferably, the DNA sequence of the endogenous GPCR is used to make a probe for either radiolabeled cDNA or RT-PCR identification of the expression of the GPCR in tissue samples.

- 15 The presence of a receptor in a diseased tissue, or the presence of the receptor at elevated or decreased concentrations in diseased tissue compared to a normal tissue, can be preferably utilized to identify a correlation with that disease. Receptors can equally well be localized to regions of organs by this technique. Based on the known functions of the specific tissues to which the receptor is localized, the putative functional role of the receptor can be deduced.

20 **C. A "Human GPCR Proline Marker" Algorithm and the Creation of Non-Endogenous, Constitutively-Active Human GPCRs**

Among the many challenges facing the biotechnology arts is the unpredictability in gleaning genetic information from one species and correlating that information to another species

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– nowhere in this art does this problem evidence more annoying exacerbation than in the genetic sequences that encode nucleic acids and proteins. Thus, for consistency and because of the highly unpredictable nature of this art, the following invention is limited, in terms of mammals, to human GPCRs – applicability of this invention to other mammalian species, while a potential possibility, is considered beyond mere rote application.

In general, when attempting to apply common "rules" from one related protein sequence to another or from one species to another, the art has typically resorted to sequence alignment, *i.e.*, sequences are linearized and attempts are then made to find regions of commonality between two or more sequences. While useful, this approach does not always prove to result in meaningful information. In the case of GPCRs, while the general structural motif is identical for all GPCRs, the variations in lengths of the TMs, ECs and ICs make such alignment approaches from one GPCR to another difficult at best. Thus, while it may be desirable to apply a consistent approach to, *e.g.*, constitutive activation from one GPCR to another, because of the great diversity in sequence length, fidelity, etc from one GPCR to the next, a generally applicable, and readily successful mutational alignment approach is in essence not possible. In an analogy, such an approach is akin to having a traveler start a journey at point A by giving the traveler dozens of different maps to point B, without any scale or distance markers on any of the maps, and then asking the traveler to find the shortest and most efficient route to destination B only by using the maps. In such a situation, the task can be readily simplified by having (a) a common "place-marker" on each map, and (b) the ability to measure the distance from the place-marker to destination B – this, then, will allow the traveler to select the most efficient from starting-point A to destination B.

In essence, a feature of the invention is to provide such coordinates within human GPCRs

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that readily allows for creation of a constitutively active form of the human GPCRs.

As those in the art appreciate, the transmembrane region of a cell is highly hydrophobic; thus, using standard hydrophobicity plotting techniques, those in the art are readily able to determine the TM regions of a GPCR, and specifically TM6 (this same approach is also
5 applicable to determining the EC and IC regions of the GPCR). It has been discovered that within the TM6 region of human GPCRs, a common proline residue (generally near the middle of TM6), acts as a constitutive activation "marker." By counting 15 amino acids from the proline marker, the 16th amino acid (which is located in the IC3 loop), when mutated from its endogenous form to a non-endogenous form, leads to constitutive activation of the receptor. For convenience, we
10 refer to this as the "Human GPCR Proline Marker" Algorithm. Although the non-endogenous amino acid at this position can be any of the amino acids, most preferably, the non-endogenous amino acid is lysine. While not wishing to be bound by any theory, we believe that this position itself is unique and that the mutation at this location impacts the receptor to allow for constitutive activation.

15 We note that, for example, when the endogenous amino acid at the 16th position is already lysine (as is the case with GPR4 and GPR32), then in order for X to be a non-endogenous amino acid, it must be other than lysine; thus, in those situations where the endogenous GPCR has an endogenous lysine residue at the 16th position, the non-endogenous version of that GPCR preferably incorporates an amino acid other than lysine, preferably alanine, histidine and arginine,
20 at this position. Of further note, it has been determined that GPR4 appears to be linked to Gs and active in its endogenous form (data not shown).

Because there are only 20 naturally occurring amino acids (although the use of non-naturally occurring amino acids is also viable), selection of a particular non-endogenous amino

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acid for substitution at this 16th position is viable and allows for efficient selection of a non-endogenous amino acid that fits the needs of the investigator. However, as noted, the more preferred non-endogenous amino acids at the 16th position are lysine, histidine, arginine and alanine, with lysine being most preferred. Those of ordinary skill in the art are credited with the ability to readily determine proficient methods for changing the sequence of a codon to achieve a desired mutation.

It has also been discovered that occasionally, but not always, the proline residue marker will be preceded in TM6 by W2 (*i.e.*, W2P¹AA₁₅X) where W is tryptophan and 2 is any amino acid residue.

Our discovery, amongst other things, negates the need for unpredictable and complicated sequence alignment approaches commonly used by the art. Indeed, the strength of our discovery, while an algorithm in nature, is that it can be applied in a facile manner to human GPCRs, with dexterous simplicity by those in the art, to achieve a unique and highly useful end-product, *i.e.*, a constitutively activated version of a human GPCR. Because many years and significant amounts of money will be required to determine the endogenous ligands for the human GPCRs that the Human Genome project is uncovering, the disclosed invention not only reduces the time necessary to positively exploit this sequence information, but at significant cost-savings. This approach truly validates the importance of the Human Genome Project because it allows for the utilization of genetic information to not only understand the role of the GPCRs in, *e.g.*, diseases, but also provides the opportunity to improve the human condition.

D. Screening of Candidate Compounds

1. Generic GPCR screening assay techniques

When a G protein receptor becomes constitutively active, it couples to a G protein (*e.g.*,

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Gq, Gs, Gi, Go) and stimulates release and subsequent binding of GTP to the G protein. The G protein then acts as a GTPase and slowly hydrolyzes the GTP to GDP, whereby the receptor, under normal conditions, becomes deactivated. However, constitutively activated receptors, including the non-endogenous, human constitutively active GPCRs of the present invention, continue to exchange GDP for GTP. A non-hydrolyzable analog of GTP, [³⁵S]GTPγS, can be used to monitor enhanced binding to G proteins present on membranes which express constitutively activated receptors. It is reported that [³⁵S]GTPγS can be used to monitor G protein coupling to membranes in the absence and presence of ligand. An example of this monitoring, among other examples well-known and available to those in the art, was reported by Traynor and Nahorski in 1995. The preferred use of this assay system is for initial screening of candidate compounds because the system is generically applicable to all G protein-coupled receptors regardless of the particular G protein that interacts with the intracellular domain of the receptor.

B 2. Specific GPCR screening assay techniques

C Once candidate compounds are identified using the "generic" G protein-coupled receptor assay (*i.e.*, an assay to select compounds that are agonists, partial agonists, or inverse agonists), further screening to confirm that the compounds have interacted at the receptor site is preferred. For example, a compound identified by the "generic" assay may not bind to the receptor, but may instead merely "uncouple" the G protein from the intracellular domain.

20 a. Gs and Gi.

Gs stimulates the enzyme adenylyl cyclase. Gi (and Go), on the other hand, inhibit this enzyme. Adenylyl cyclase catalyzes the conversion of ATP to cAMP; thus,

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constitutively activated GPCRs that couple the Gs protein are associated with increased cellular levels of cAMP. On the other hand, constitutively activated GPCRs that couple the Gi (or Go) protein are associated with decreased cellular levels of cAMP. *See, generally, "Indirect Mechanisms of Synaptic Transmission," Chpt. 8, From Neuron To Brain (3rd Ed.)*

5 Nichols, J.G. et al eds. Sinauer Associates, Inc. (1992). Thus, assays that detect cAMP can be utilized to determine if a candidate compound is, *e.g.*, an inverse agonist to the receptor (*i.e.*, such a compound would decrease the levels of cAMP). A variety of approaches known in the art for measuring cAMP can be utilized; a most preferred approach relies upon the use of anti-cAMP antibodies in an ELISA-based format. Another type of assay that can be

10 utilized is a whole cell second messenger reporter system assay. Promoters on genes drive the expression of the proteins that a particular gene encodes. Cyclic AMP drives gene expression by promoting the binding of a cAMP-responsive DNA binding protein or transcription factor (CREB) which then binds to the promoter at specific sites called cAMP response elements and drives the expression of the gene. Reporter systems can be constructed which have a promoter containing

15 multiple cAMP response elements before the reporter gene, *e.g.*, β -galactosidase or luciferase. Thus, a constitutively activated Gs-linked receptor causes the accumulation of cAMP that then activates the gene and expression of the reporter protein. The reporter protein such as β -galactosidase or luciferase can then be detected using standard biochemical assays (Chen et al. 1995). With respect to GPCRs that link to Gi (or Go), and thus decrease levels of cAMP, an

20 approach to the screening of, *e.g.*, inverse agonists, based upon utilization of receptors that link to Gs (and thus increase levels of cAMP) is disclosed in the Example section with respect to GPR17 and GPR30.

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b. Go and Gq.

Gq and Go are associated with activation of the enzyme phospholipase C, which in turn hydrolyzes the phospholipid PIP_2 , releasing two intracellular messengers: diacylglycerol (DAG) and inistol 1,4,5-triphoisphate (IP_3). Increased accumulation of IP_3 is associated with activation of Gq- and Go-associated receptors. *See, generally*, "Indirect Mechanisms of Synaptic Transmission," Chpt. 8, From Neuron To Brain (3rd Ed.) Nichols, J.G. et al eds. Sinauer Associates, Inc. (1992). Assays that detect IP_3 accumulation can be utilized to determine if a candidate compound is, *e.g.*, an inverse agonist to a Gq- or Go-associated receptor (*i.e.*, such a compound would decrease the levels of IP_3). Gq-associated receptors can also been examined using an AP1 reporter assay in that Gq-dependent phospholipase C causes activation of genes containing AP1 elements; thus, activated Gq-associated receptors will evidence an increase in the expression of such genes, whereby inverse agonists thereto will evidence a decrease in such expression, and agonists will evidence an increase in such expression. Commercially available assays for such detection are available.

E. Medicinal Chemistry

Generally, but not always, direct identification of candidate compounds is preferably conducted in conjunction with compounds generated via combinatorial chemistry techniques, whereby thousands of compounds are randomly prepared for such analysis. Generally, the results of such screening will be compounds having unique core structures; thereafter, these compounds are preferably subjected to additional chemical modification around a preferred core structure(s) to further enhance the medicinal properties thereof. Such techniques are

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known to those in the art and will not be addressed in detail in this patent document.

F. Pharmaceutical Compositions

Candidate compounds selected for further development can be formulated into pharmaceutical compositions using techniques well known to those in the art. Suitable
5 pharmaceutically-acceptable carriers are available to those in the art; for example, *see* Remington's Pharmaceutical Sciences, 16th Edition, 1980, Mack Publishing Co., (Oslo et al., eds.)

G. Other Utility

Although a preferred use of the non-endogenous versions of the disclosed human GPCRs is for the direct identification of candidate compounds as inverse agonists, agonists or partial
10 agonists (preferably for use as pharmaceutical agents), these receptors can also be utilized in research settings. For example, in vitro and in vivo systems incorporating these receptors can be utilized to further elucidate and understand the roles of the receptors in the human condition, both normal and diseased, as well understanding the role of constitutive activation as it applies to understanding the signaling cascade. A value in these non-endogenous receptors is that their
15 utility as a research tool is enhanced in that, because of their unique features, the disclosed receptors can be used to understand the role of a particular receptor in the human body before the endogenous ligand therefor is identified. Other uses of the disclosed receptors will become apparent to those in the art based upon, *inter alia*, a review of this patent document.

EXAMPLES

20 The following examples are presented for purposes of elucidation, and not limitation, of the present invention. Following the teaching of this patent document that a mutational cassette may be utilized in the IC3 loop of human GPCRs based upon a position relative to a proline residue in TM6 to constitutively activate the receptor, and while specific nucleic acid

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and amino acid sequences are disclosed herein, those of ordinary skill in the art are credited with the ability to make minor modifications to these sequences while achieving the same or substantially similar results reported below. Particular approaches to sequence mutations are within the purview of the artisan based upon the particular needs of the artisan.

5 **Example 1**
Preparation of Endogenous Human GPCRs

A variety of GPCRs were utilized in the Examples to follow. Some endogenous human GPCRs were graciously provided in expression vectors (as acknowledged below) and other endogenous human GPCRs were synthesized *de novo* using publicly-available sequence
10 information.

1. **GPR1 (GenBank Accession Number: U13666)**

The human cDNA sequence for GPR1 was provided in pRcCMV by Brian O'Dowd (University of Toronto). GPR1 cDNA (1.4kB fragment) was excised from the pRcCMV vector as a NdeI-XbaI fragment and was subcloned into the NdeI-XbaI site of pCMV vector (*see*
15 Figure 3). Nucleic acid (SEQ.ID.NO.: 1) and amino acid (SEQ.ID.NO.: 2) sequences for human GPR1 were thereafter determined and verified.

2. **GPR4 (GenBank Accession Numbers: L36148, U35399, U21051)**

The human cDNA sequence for GPR4 was provided in pRcCMV by Brian O'Dowd (University of Toronto). GPR1 cDNA (1.4kB fragment) was excised from the pRcCMV
20 vector as an ApaI(blunted)-XbaI fragment and was subcloned (with most of the 5' untranslated region removed) into HindIII(blunted)-XbaI site of pCMV vector. Nucleic acid (SEQ.ID.NO.: 3) and amino acid (SEQ.ID.NO.: 4) sequences for human GPR4 were thereafter determined and verified.

3. **GPR5 (GenBank Accession Number: L36149)**

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The cDNA for human GPR5 was generated and cloned into pCMV expression vector as follows: PCR was performed using genomic DNA as template and rTth polymerase (Perkin Elmer) with the buffer system provided by the manufacturer, 0.25 μ M of each primer, and 0.2 mM of each of the 4 nucleotides. The cycle condition was 30 cycles of: 94°C for 1 min; 64°C for 1min; and 72°C for 1.5 min. The 5' PCR primer contained an EcoRI site with the sequence: 5'-TATGAATTCAGATGCTCTAAACGTCCCTGC-3' (SEQ.ID.NO.: 5) and the 3' primer contained BamHI site with the sequence: 5'-TCCGGATCCACCTGCACCTGCGCCTGCACC-3' (SEQ.ID.NO.: 6). The 1.1 kb PCR fragment was digested with EcoRI and BamHI and cloned into EcoRI-BamHI site of pCMV expression vector. Nucleic acid (SEQ.ID.NO.: 7) and amino acid (SEQ.ID.NO.: 8) sequences for human GPR5 were thereafter determined and verified.

4. GPR7 (GenBank Accession Number: U22491)

The cDNA for human GPR7 was generated and cloned into pCMV expression vector as follows: PCR condition- PCR was performed using genomic DNA as template and rTth polymerase (Perkin Elmer) with the buffer system provided by the manufacturer, 0.25 μ M of each primer, and 0.2 mM of each of the 4 nucleotides. The cycle condition was 30 cycles of: 94°C for 1 min; 62°C for 1min; and 72°C for 1min and 20 sec. The 5' PCR primer contained a HindIII site with the sequence: 5'-GCAAGCTTGGGGGACGCCAGGTCGCCGGCT-3' (SEQ.ID.NO.: 9) and the 3' primer contained a BamHI site with the sequence: 5'-GCGGATCCGGACGCTGGGGGAGTCAGGCTGC-3' (SEQ.ID.NO.: 10). The 1.1 kb PCR fragment was digested with HindIII and BamHI and cloned into HindIII-BamHI site of pCMV expression vector. Nucleic acid (SEQ.ID.NO.: 11) and amino acid (SEQ.ID.NO.:

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12) sequences for human GPR7 were thereafter determined and verified.

5. GPR8 (GenBank Accession Number: U22492)

The cDNA for human GPR8 was generated and cloned into pCMV expression vector as follows: PCR was performed using genomic DNA as template and rTth polymerase
5 (Perkin Elmer) with the buffer system provided by the manufacturer, 0.25 μ M of each primer, and 0.2 mM of each of the 4 nucleotides. The cycle condition was 30 cycles of: 94°C for 1 min; 62°C for 1min; and 72 °C for 1min and 20 sec. The 5' PCR primer contained an EcoRI site with the sequence:

5'-CGGAATTCGTCAACGGTCCCAGCTACAATG-3' (SEQ.ID.NO.: 13).

10 and the 3' primer contained a BamHI site with the sequence:

5'-ATGGATCCCAGGCCCTTCAGCACCGCAATAT-3'(SEQ.ID.NO.: 14).

The 1.1 kb PCR fragment was digested with EcoRI and BamHI and cloned into EcoRI-BamHI site of PCMV expression vector. All 4 cDNA clones sequenced contained a possible polymorphism involving a change of amino acid 206 from Arg to Gln. Aside from this
15 difference, nucleic acid (SEQ.ID.NO.: 15) and amino acid (SEQ.ID.NO.: 16) sequences for human GPR8 were thereafter determined and verified.

6. GPR9 (GenBank Accession Number: X95876)

The cDNA for human GPR9 was generated and cloned into pCMV expression vector as follows: PCR was performed using a clone (provided by Brian O'Dowd) as template and
20 pfu polymerase (Stratagene) with the buffer system provided by the manufacturer supplemented with 10% DMSO, 0.25 μ M of each primer, and 0.5 mM of each of the 4 nucleotides. The cycle condition was 25 cycles of: 94°C for 1 min; 56°C for 1min; and 72 °C for 2.5 min. The 5' PCR primer contained an EcoRI site with the sequence:

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5'-ACGAATTCAGCCATGGTCCTTGAGGTGAGTGACCACCAAGTGCTAAAT-3'

(SEQ.ID.NO.: 17)

and the 3' primer contained a BamHI site with the sequence:

5'-GAGGATCCTGGAATGCGGGGAAGTCAG-3' (SEQ.ID.NO.: 18).

- 5 The 1.2 kb PCR fragment was digested with EcoRI and cloned into EcoRI-SmaI site of pCMV expression vector. Nucleic acid (SEQ.ID.NO.: 19) and amino acid (SEQ.ID.NO.: 20) sequences for human GPR9 were thereafter determined and verified.

7. GPR9-6 (GenBank Accession Number: U45982)

- The cDNA for human GPR9-6 was generated and cloned into pCMV expression
10 vector as follows: PCR was performed using genomic DNA as template and rTth polymerase (Perkin Elmer) with the buffer system provided by the manufacturer, 0.25 µM of each primer, and 0.2 mM of each of the 4 nucleotides. The cycle condition was 30 cycles of: 94°C for 1 min; 62°C for 1min; and 72°C for 1 min and 20 sec. The 5' PCR primer was kinased with the sequence:

5'-TTAAGCTTGACCTAATGCCATCTTGTGTCC-3' (SEQ.ID.NO.: 21)

- 15 and the 3' primer contained a BamHI site with the sequence:

5'-TTGGATCCAAAAGAACCATGCACCTCAGAG-3' (SEQ.ID.NO.: 22).

The 1.2 kb PCR fragment was digested with BamHI and cloned into EcoRV-BamHI site of pCMV expression vector. Nucleic acid (SEQ.ID.NO.: 23) and amino acid (SEQ.ID.NO.: 24) sequences for human GPR9-6 were thereafter determined and verified.

20 **8. GPR10 (GenBank Accession Number: U32672)**

The human cDNA sequence for GPR10 was provided in pRcCMV by Brian O'Dowd (University of Toronto). GPR10 cDNA (1.3kB fragment) was excised from the pRcCMV vector as an EcoRI-XbaI fragment and was subcloned into EcoRI-XbaI site of pCMV

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vector. Nucleic acid (SEQ.ID.NO.: 25) and amino acid (SEQ.ID.NO.: 26) sequences for human GPR10 were thereafter determined and verified.

9. GPR15 (GenBank Accession Number: U34806)

The human cDNA sequence for GPR15 was provided in pCDNA3 by Brian
5 O'Dowd (University of Toronto). GPR15 cDNA (1.5kB fragment) was excised from the pCDNA3 vector as a HindIII-Bam fragment and was subcloned into HindIII-Bam site of pCMV vector. Nucleic acid (SEQ.ID.NO.: 27) and amino acid (SEQ.ID.NO.: 28) sequences for human GPR15 were thereafter determined and verified.

10. GPR17 (GenBank Accession Number: Z94154)

10 The cDNA for human GPR17 was generated and cloned into pCMV expression vector as follows: PCR was performed using genomic DNA as template and rTth polymerase (Perkin Elmer) with the buffer system provided by the manufacturer, 0.25 μ M of each primer, and 0.2 mM of each 4 nucleotides. The cycle condition was 30 cycles of: 94°C for 1 min; 56°C for 1min and 72 °C for 1 min and 20 sec. The 5' PCR primer contained an EcoRI site with the
15 sequence:

5'-CTAGAATTCTGACTCCAGCCAAAGCATGAAT-3' (SEQ.ID.NO.: 29) and the 3' primer contained a BamHI site with the sequence:

5'-GCTGGATCCTAAACAGTCTGCGCTCGGCCT-3' (SEQ.ID.NO.: 30).

The 1.1 kb PCR fragment was digested with EcoRI and BamHI and cloned into EcoRI-BamHI
20 site of pCMV expression vector. Nucleic acid (SEQ.ID.NO.: 31) and amino acid (SEQ.ID.NO.: 32) sequences for human GPR17 were thereafter determined and verified.

11. GPR18 (GenBank Accession Number: L42324)

The cDNA for human GPR18 was generated and cloned into pCMV expression

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vector as follows: PCR was performed using genomic DNA as template and rTth polymerase (Perkin Elmer) with the buffer system provided by the manufacturer, 0.25 μ M of each primer, and 0.2 mM of each of the 4 nucleotides. The cycle condition was 30 cycles of: 94°C for 1 min; 54°C for 1min; and 72 °C for 1min and 20 sec. The 5' PCR primer was kinased with the sequence:

5 5'-ATAAGATGATCACCTGAACAATCAAGAT -3' (SEQ.ID.NO.: 33)

and the 3' primer contained an EcoRI site with the sequence:

5'-TCCGAATTCATAACATTTCACTGTTTATATTGC-3' (SEQ.ID.NO.: 34).

The 1.0 kb PCR fragment was digested with EcoRI and cloned into blunt-EcoRI site of pCMV expression vector. All 8 cDNA clones sequenced contained 4 possible polymorphisms involving
10 changes of amino acid 12 from Thr to Pro, amino acid 86 from Ala to Glu, amino acid 97 from Ile to Leu and amino acid 310 from Leu to Met. Aside from these changes, nucleic acid (SEQ.ID.NO.: 35) and amino acid (SEQ.ID.NO.: 36) sequences for human GPR18 were thereafter determined and verified.

12. GPR20 (GenBank Accession Number: U66579)

15 The cDNA for human GPR20 was generated and cloned into pCMV expression vector as follows: PCR was performed using genomic DNA as template and rTth polymerase (Perkin Elmer) with the buffer system provided by the manufacturer, 0.25 μ M of each primer, and 0.2 mM of each of the 4 nucleotides. The cycle condition was 30 cycles of: 94°C for 1 min; 62°C for 1min; and 72 °C for 1 min and 20 sec. The 5' PCR primer was kinased with the sequence:

20 5'-CCAAGCTTCCAGGCCTGGGGTGTGCTGG-3' (SEQ.ID.NO.: 37)

and the 3' primer contained a BamHI site with the sequence:

5'-ATGGATCCTGACCTTCGGCCCCTGGCAGA-3' (SEQ.ID.NO.: 38).

The 1.2 kb PCR fragment was digested with BamHI and cloned into EcoRV-BamHI site of

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PCMV expression vector. Nucleic acid (SEQ.ID.NO.: 39) and amino acid (SEQ.ID.NO.: 40) sequences for human GPR20 were thereafter determined and verified.

13. GPR21 (GenBank Accession Number: U66580)

The cDNA for human GPR21 was generated and cloned into pCMV expression
5 vector as follows: PCR was performed using genomic DNA as template and rTth polymerase (Perkin Elmer) with the buffer system provided by the manufacturer, 0.25 μ M of each primer, and 0.2 mM of each of the 4 nucleotides. The cycle condition was 30 cycles of: 94°C for 1 min; 62°C for 1min; and 72°C for 1 min and 20 sec. The 5' PCR primer was kinased with the sequence:
5'-GAGAATTCACCTCCTGAGCTCAAGATGAACT-3' (SEQ.ID.NO.: 41)

10 and the 3' primer contained a BamHI site with the sequence:

5'-CGGGATCCCCGTAAGTGAAGTCAAGAT-3' (SEQ.ID.NO.: 42).

The 1.1 kb PCR fragment was digested with BamHI and cloned into EcoRV-BamHI site of pCMV expression vector. Nucleic acid (SEQ.ID.NO.: 43) and amino acid (SEQ.ID.NO.: 44) sequences for human GPR21 were thereafter determined and verified.

15 14. GPR22 (GenBank Accession Number: U66581)

The cDNA for human GPR22 was generated and cloned into pCMV expression
vector as follows: PCR was performed using genomic DNA as template and rTth polymerase (Perkin Elmer) with the buffer system provided by the manufacturer, 0.25 μ M of each primer, and 0.2 mM of each of the 4 nucleotides. The cycle condition was 30 cycles of: 94°C for 1 min; 50°C
20 for 1min; and 72°C for 1.5 min. The 5' PCR primer was kinased with the sequence:

5'-TCCCCCGGGAAAAAACAAGTCTCCAAA-3' (SEQ.ID.NO.: 45)

and the 3' primer contained a BamHI site with the sequence:

5'-TAGGATCCATTTGAATGTGGATTTGGTGAAG-3' (SEQ.ID.NO.: 46).

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The 1.38 kb PCR fragment was digested with BamHI and cloned into EcoRV-BamHI site of pCMV expression vector. Nucleic acid (SEQ.ID.NO.: 47) and amino acid (SEQ.ID.NO.: 48) sequences for human GPR22 were thereafter determined and verified.

15. GPR24 (GenBank Accession Number: U71092)

5 The cDNA for human GPR24 was generated and cloned into pCMV expression vector as follows: PCR was performed using genomic DNA as template and rTth polymerase (Perkin Elmer) with the buffer system provided by the manufacturer, 0.25 μ M of each primer, and 0.2 mM of each 4 nucleotides. The cycle condition was 30 cycles of: 94°C for 1 min; 56°C for 1min; and 72 °C for 1 min and 20 sec. The 5' PCR primer contains a HindIII site with the
10 sequence:

5'-GTGAAGCTTGCCTCTGGTGCCTGCAGGAGG-3' (SEQ.ID.NO.: 49)

and the 3' primer contains an EcoRI site with the sequence:

5'-GCAGAAATCCCGGTGGCGTGTGTGGTGCCC-3' (SEQ.ID.NO.: 50).

The 1.3 kb PCR fragment was digested with HindIII and EcoRI and cloned into HindIII-EcoRI
15 site of pCMV expression vector. The nucleic acid (SEQ.ID.NO.: 51) and amino acid sequence (SEQ.ID.NO.: 52) for human GPR24 were thereafter determined and verified.

16. GPR30 (GenBank Accession Number: U63917)

The cDNA for human GPR30 was generated and cloned as follows: the coding sequence of GPR30 (1128bp in length) was amplified from genomic DNA using the primers:

20 5'-GGCGGATCCATGGATGTGACTTCCCAA-3' (SEQ.ID.NO.: 53) and

5'-GGCGGATCCCTACACGGCACTGCTGAA-3' (SEQ.ID.NO.: 54).

The amplified product was then cloned into a commercially available vector, pCR2.1 (Invitrogen),

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using a "TOPO-TA Cloning Kit" (Invitrogen, #K4500-01), following manufacturer instructions. The full-length GPR30 insert was liberated by digestion with BamHI, separated from the vector by agarose gel electrophoresis, and purified using a Sephaglas Bandprep™ Kit (Pharmacia, # 27-9285-01) following manufacturer instructions. The nucleic acid (SEQ.ID.NO.: 55) and amino acid
5 sequence (SEQ.ID.NO.: 56) for human GPR30 were thereafter determined and verified.

17. GPR31 (GenBank Accession Number: U65402)

The cDNA for human GPR31 was generated and cloned into pCMV expression vector as follows: PCR was performed using genomic DNA as template and rTth polymerase (Perkin Elmer) with the buffer system provided by the manufacturer, 0.25 μM of each primer, and
10 0.2 mM of each of the 4 nucleotides. The cycle condition was 30 cycles of: 94°C for 1 min; 58°C for 1min; and 72 °C for 2 min. The 5' PCR primer contained an EcoRI site with the sequence:
5'-AAGGAATTCACGGCCGGGTGATGCCATTCCC-3' (SEQ.ID.NO.: 57)
and the 3' primer contained a BamHI site with the sequence:
5'-GGTGGATCCATAAACACGGGCGTTGAGGAC -3' (SEQ.ID.NO.: 58).
15 The 1.0 kb PCR fragment was digested with EcoRI and BamHI and cloned into EcoRI-BamHI site of pCMV expression vector. Nucleic acid (SEQ.ID.NO.: 59) and amino acid (SEQ.ID.NO.: 60) sequences for human GPR31 were thereafter determined and verified.

18. GPR32 (GenBank Accession Number: AF045764)

The cDNA for human GPR32 was generated and cloned into pCMV expression
20 vector as follows: PCR was performed using genomic DNA as template and rTth polymerase (Perkin Elmer) with the buffer system provided by the manufacturer, 0.25 μM of each primer, and 0.2 mM of each 4 nucleotides. The cycle condition was 30 cycles of: 94°C for 1 min; 56°C for 1min; and 72 °C for 1 min and 20 sec. The 5' PCR primer contained an EcoRI site with the

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sequence:

5'-TAAGAATTCCATAAAAAATTATGGAATGG-3' (SEQ.ID.NO.:243)

and the 3' primer contained a BamHI site with the sequence:

5'-CCAGGATCCAGCTGAAGTCTTCATCATT-3' (SEQ.ID.NO.: 244).

- 5 The 1.1 kb PCR fragment was digested with EcoRI and BamHI and cloned into EcoRI-BamHI site of pCMV expression vector. Nucleic acid (SEQ.ID.NO.: 245) and amino acid (SEQ.ID.NO.: 246) sequences for human GPR32 were thereafter determined and verified.

19. GPR40 (GenBank Accession Number: AF024687)

- The cDNA for human GPR40 was generated and cloned into pCMV expression
10 vector as follows: PCR was performed using genomic DNA as template and rTth polymerase (Perkin Elmer) with the buffer system provided by the manufacturer, 0.25 μ M of each primer, and 0.2 mM of each 4 nucleotides. The cycle condition was 30 cycles of: 94°C for 1 min, 65°C for 1min and 72 °C for 1 min and 10 sec. The 5' PCR primer contained an EcoRI site with the sequence

- 15 5'-GCAGAATTCGGCGGCCCCATGGACCTGCCCCC-3' (SEQ.ID.NO.: 247)

and the 3' primer contained a BamHI site with the sequence

5'-GCTGGATCCCCGAGCAGTGGCGTTACTTC-3' (SEQ.ID.NO.: 248).

- The 1 kb PCR fragment was digested with EcoRI and BamHI and cloned into EcoRI-BamHI site of pCMV expression vector. Nucleic acid (SEQ.ID.NO.: 249) and amino acid (SEQ.ID.NO.: 250)
20 sequences for human GPR40 were thereafter determined and verified.

20. GPR41 (GenBank Accession Number AF024688)

The cDNA for human GPR41 was generated and cloned into pCMV expression vector as follows: PCR was performed using genomic DNA as template and rTth polymerase

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(Perkin Elmer) with the buffer system provided by the manufacturer, 0.25 μ M of each primer, and 0.2 mM of each 4 nucleotides. The cycle condition was 30 cycles of 94°C for 1 min, 65°C for 1min and 72 °C for 1 min and 10 sec. The 5' PCR primer contained an HindIII site with the sequence:

5 5'-CTCAAGCTTACTCTCTCTCACCAGTGGCCAC-3' (SEQ.ID.NO.: 251)

and the 3' primer was kinased with the sequence

5'-CCCTCCTCCCCCGGAGGACCTAGC-3' (SEQ.ID.NO.: 252).

The 1 kb PCR fragment was digested with HindIII and cloned into HindIII-blunt site of pCMV expression vector. Nucleic acid (SEQ.ID.NO.: 253) and amino acid (SEQ.ID.NO.: 254)

10 sequences for human GPR41 were thereafter determined and verified.

21. GPR43 (GenBank Accession Number AF024690)

The cDNA for human GPR43 was generated and cloned into pCMV expression vector as follows: PCR was performed using genomic DNA as template and rTth polymerase (Perkin Elmer) with the buffer system provided by the manufacturer, 0.25 μ M of each primer, and
15 0.2 mM of each 4 nucleotides. The cycle condition was 30 cycles of: 94°C for 1 min; 65°C for 1min; and 72 °C for 1 min and 10 sec. The 5' PCR primer contains an HindIII site with the sequence:

5'-TTTAAGCTTCCCCTCCAGGATGCTGCCGGAC-3' (SEQ.ID.NO.: 255)

and the 3' primer contained an EcoRI site with the sequence:

20 5'-GGCGAATTCTGAAGGTCCAGGGAAACTGCTA-3' (SEQ.ID.NO. 256).

The 1 kb PCR fragment was digested with HindIII and EcoRI and cloned into HindIII-EcoRI site of pCMV expression vector. Nucleic acid (SEQ.ID.NO.: 257) and amino acid (SEQ.ID.NO.: 258) sequences for human GPR43 were thereafter determined and verified.

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22. APJ (GenBank Accession Number: U03642)

Human APJ cDNA (in pRcCMV vector) was provided by Brian O'Dowd (University of Toronto). The human APJ cDNA was excised from the pRcCMV vector as an EcoRI-XbaI (blunted) fragment and was subcloned into EcoRI-SmaI site of pCMV vector.

- 5 Nucleic acid (SEQ.ID.NO.: 61) and amino acid (SEQ.ID.NO.: 62) sequences for human APJ were thereafter determined and verified.

23. BLR1 (GenBank Accession Number: X68149)

The cDNA for human BLR1 was generated and cloned into pCMV expression vector as follows: PCR was performed using thymus cDNA as template and rTth polymerase
10 (Perkin Elmer) with the buffer system provided by the manufacturer, 0.25 μ M of each primer, and 0.2 mM of each of the 4 nucleotides. The cycle condition was 30 cycles of: 94°C for 1 min; 62°C for 1min; and 72°C for 1 min and 20 sec. The 5' PCR primer contained an EcoRI site with the sequence:

5'-TGAGAATTCTGGTGACTCACAGCCGGCACAG-3' (SEQ.ID.NO.: 63):

- 15 and the 3' primer contained a BamHI site with the sequence:

5'-GCCGGATCCAAGGAAAAGCAGCAATAAAAGG-3' (SEQ.ID.NO.: 64). The 1.2 kb PCR fragment was digested with EcoRI and BamHI and cloned into EcoRI-BamHI site of pCMV expression vector. Nucleic acid (SEQ.ID.NO.: 65) and amino acid (SEQ.ID.NO.: 66) sequences for human BLR1 were thereafter determined and verified.

20 **24. CEPR (GenBank Accession Number: U77827)**

The cDNA for human CEPR was generated and cloned into pCMV expression vector as follows: PCR was performed using genomic DNA as template and rTth polymerase (Perkin Elmer) with the buffer system provided by the manufacturer, 0.25 μ M of each primer, and

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0.2 mM of each of the 4 nucleotides. The cycle condition was 30 cycles of: 94°C for 1 min; 65°C for 1min; and 72 °C for 1 min and 20 sec. The 5' PCR primer was kinased with the sequence:

5'-CAAAGCTTGAAAGCTGCACGGTGCAGAGAC-3' (SEQ.ID.NO.:67)

and the 3' primer contained a BamHI site with the sequence:

5'-GCGGATCCCGAGTCACACCCTGGCTGGGCC-3' (SEQ.ID.NO.: 68).

The 1.2 kb PCR fragment was digested with BamHI and cloned into EcoRV-BamHI site of pCMV expression vector. Nucleic acid (SEQ.ID.NO.: 69) and amino acid (SEQ.ID.NO.: 70) sequences for human CEPR were thereafter determined and verified.

25. EBI1 (GenBank Accession Number: L31581)

The cDNA for human EBI1 was generated and cloned into pCMV expression vector as follows: PCR was performed using thymus cDNA as template and rTth polymerase (Perkin Elmer) with the buffer system provided by the manufacturer, 0.25 µM of each primer, and 0.2 mM of each of the 4 nucleotides. The cycle condition was 30 cycles of: 94°C for 1 min; 62°C for 1min; and 72 °C for 1 min and 20 sec. The 5' PCR primer contained an EcoRI site with the sequence:

5'-ACAGAATTCCTGTGTGGTTTTACCGCCCAG-3' (SEQ.ID.NO.: 71)

and the 3' primer contained a BamHI site with the sequence:

5'-CTCGGATCCAGGCAGAAGAGTCGCCTATGG-3' (SEQ.ID.NO.: 72).

The 1.2 kb PCR fragment was digested with EcoRI and BamHI and cloned into EcoRI-BamHI site of pCMV expression vector. Nucleic acid (SEQ.ID.NO.: 73) and amino acid (SEQ.ID.NO.: 74) sequences for human EBI1 were thereafter determined and verified.

26. EBI2 (GenBank Accession Number: L08177)

The cDNA for human EBI2 was generated and cloned into pCMV expression

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vector as follows: PCR was performed using cDNA clone (graciously provided by Kevin Lynch, University of Virginia Health Sciences Center; the vector utilized was not identified by the source) as template and pfu polymerase (Stratagene) with the buffer system provided by the manufacturer supplemented with 10% DMSO, 0.25 μ M of each primer, and 0.5 mM of each of the 4 nucleotides. The cycle condition was 30 cycles of: 94°C for 1 min; 60°C for 1min; and 72°C for 1 min and 20 sec. The 5' PCR primer contained an EcoRI site with the sequence:

5'-CTGGAATTCACCTGGACCACCACCAATGGATA-3' (SEQ.ID.NO.: 75)

and the 3' primer contained a BamHI site with the sequence

5'-CTCGGATCCTGCAAAGTTTGTACATACAG TT-3' (SEQ.ID.NO.: 76).

10 The 1.2 kb PCR fragment was digested with EcoRI and BamHI and cloned into EcoRI-BamHI site of pCMV expression vector. Nucleic acid (SEQ.ID.NO.: 77) and amino acid (SEQ.ID.NO.: 78) sequences for human EBI2 were thereafter determined and verified.

27. ETBR-LP2 (GenBank Accession Number: D38449)

The cDNA for human ETBR-LP2 was generated and cloned into pCMV
15 expression vector as follows: PCR was performed using brain cDNA as template and rTth polymerase (Perkin Elmer) with the buffer system provided by the manufacturer, 0.25 μ M of each primer, and 0.2 mM of each of the 4 nucleotides. The cycle condition was 30 cycles of: 94°C for 1 min; 65°C for 1min; and 72 °C for 1.5 min. The 5' PCR contained an EcoRI site with the sequence:

20 5'-CTGGAATTCTCCTGCTCATCCAGCCATGCGG -3' (SEQ.ID.NO.: 79)

and the 3' primer contained a BamHI site with the sequence:

5'-CCTGGATCCCCACCCCTACTGGGGCCTCAG -3' (SEQ.ID.NO.: 80).

The 1.5 kb PCR fragment was digested with EcoRI and BamHI and cloned into EcoRI-BamHI

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site of pCMV expression vector. Nucleic acid (SEQ.ID.NO.: 81) and amino acid (SEQ.ID.NO.: 82) sequences for human ETBR-LP2 were thereafter determined and verified.

28. GHSR (GenBank Accession Number: U60179)

The cDNA for human GHSR was generated and cloned into pCMV expression vector as follows: PCR was performed using hippocampus cDNA as template and TaqPlus Precision polymerase (Stratagene) with the buffer system provided by the manufacturer, 0.25 μ M of each primer, and 0.2 mM of each of the 4 nucleotides. The cycle condition was 30 cycles of: 94°C for 1 min; 68°C for 1min; and 72°C for 1 min and 10 sec. For first round PCR, the 5' PCR primer sequence was:

10 5'-ATGTGGAACGCGACGCCAGCG-3' (SEQ.ID.NO.: 83)

and the 3' primer sequence was:

5'-TCATGTATTAATACTAGATTCT-3' (SEQ.ID.NO.: 84).

Two microliters of the first round PCR was used as template for the second round PCR where the 5' primer was kinased with sequence:

15 5'-TACCATGTGGAACGCGACGCCAGCGAAGAGCCGGGGT-3'(SEQ.ID.NO.:85)

and the 3' primer contained an EcoRI site with the sequence:

5'-CGGAATTCATGTATTAATACTAGATTCTGTCCAGGCCCG-3'(SEQ.ID.NO.:86).

The 1.1 kb PCR fragment was digested with EcoRI and cloned into blunt-EcoRI site of pCMV expression vector. Nucleic acid (SEQ.ID.NO.: 87) and amino acid (SEQ.ID.NO.: 88) sequences
20 for human GHSR were thereafter determined and verified.

29. GPCR-CNS (GenBank Accession Number: AF017262)

The cDNA for human GPCR-CNS was generated and cloned into pCMV expression vector as follows: PCR was performed using brain cDNA as template and rTth

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polymerase (Perkin Elmer) with the buffer system provided by the manufacturer, 0.25 μ M of each primer, and 0.2 mM of each of the 4 nucleotides. The cycle condition was 30 cycles of: 94°C for 1 min; 65°C for 1min; and 72°C for 2 min. The 5' PCR primer contained a HindIII site with the sequence:

5 5'-GCAAGCTTGTGCCCTCACCAAGCCATGCGAGCC-3' (SEQ.ID.NO.: 89)

and the 3' primer contained an EcoRI site with the sequence:

5'-CGGAATTCAGCAATGAGTTCCGACAGAAGC-3' (SEQ.ID.NO.: 90).

The 1.9 kb PCR fragment was digested with HindIII and EcoRI and cloned into HindIII-EcoRI site of pCMV expression vector. All nine clones sequenced contained a potential polymorphism
10 involving a S284C change. Aside from this difference, nucleic acid (SEQ.ID.NO.: 91) and amino acid (SEQ.ID.NO.: 92) sequences for human GPCR-CNS were thereafter determined and verified.

30. GPR-NGA (GenBank Accession Number: U55312)

The cDNA for human GPR-NGA was generated and cloned into pCMV expression vector as follows: PCR was performed using genomic DNA as template and rTth
15 polymerase (Perkin Elmer) with the buffer system provided by the manufacturer, 0.25 μ M of each primer, and 0.2 mM of each of the 4 nucleotides. The cycle condition was 30 cycles of 94°C for 1 min, 56°C for 1min and 72°C for 1.5 min. The 5' PCR primer contained an EcoRI site with the sequence:

5'-CAGAATTCAGAGAAAAAAGTGAATATGGTTTTT-3' (SEQ.ID.NO.: 93)

20 and the 3' primer contained a BamHI site with the sequence:

5'-TTGGATCCCTGGTGCATAACAATTGAAAGAAT-3' (SEQ.ID.NO.: 94).

The 1.3 kb PCR fragment was digested with EcoRI and BamHI and cloned into EcoRI-BamHI site of pCMV expression vector. Nucleic acid (SEQ.ID.NO.: 95) and amino acid (SEQ.ID.NO.:

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96) sequences for human GPR-NGA were thereafter determined and verified.

31. H9 (GenBank Accession Number: U52219)

The cDNA for human HB954 was generated and cloned into pCMV expression vector as follows: PCR was performed using pituitary cDNA as template and rTth polymerase
5 (Perkin Elmer) with the buffer system provided by the manufacturer, 0.25 μ M of each primer, and 0.2 mM of each 4 nucleotides. The cycle condition was 30 cycles of: 94°C for 1 min, 62°C for 1min and 72 °C for 2 min. The 5' PCR primer contains a HindIII site with the sequence:

5'-GGAAAGCTTAACGATCCCCAGGAGCAACAT-3' (SEQ.ID.NO.: 97)

and the 3' primer contains a BamHI site with the sequence:

10 5'-CTGGGATCCTACGAGAGCATTTTTCACACAG-3' (SEQ.ID.NO.: 98).

The 1.9 kb PCR fragment was digested with HindIII and BamHI and cloned into HindIII-BamHI site of pCMV expression vector. When compared to the published sequences, a different isoform with 12 bp in frame insertion in the cytoplasmic tail was also identified and designated "H9b." Both isoforms contain two potential polymorphisms involving changes
15 of amino acid P320S and amino acid G448A. Isoform H9a contained another potential polymorphism of amino acid S493N, while isoform H9b contained two additional potential polymorphisms involving changes of amino acid I502T and amino acid A532T (corresponding to amino acid 528 of isoform H9a). Nucleic acid (SEQ.ID.NO.: 99) and amino acid (SEQ.ID.NO.: 100) sequences for human H9 were thereafter determined and
20 verified (in the section below, both isoforms were mutated in accordance with the Human GPCR Proline Marker Algorithm).

32. HB954 (GenBank Accession Number: D38449)

The cDNA for human HB954 was generated and cloned into pCMV expression

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vector as follows: PCR was performed using brain cDNA as template and rTth polymerase (Perkin Elmer) with the buffer system provided by the manufacturer, 0.25 μ M of each primer, and 0.2 mM of each of the 4 nucleotides. The cycle condition was 30 cycles of 94°C for 1 min, 58°C for 1 min and 72°C for 2 min. The 5' PCR contained a HindIII site with the sequence:

5 5'-TCCAAGCTTCGCCATGGGACATAACGGGAGCT-3' (SEQ.ID.NO.: 101)

and the 3' primer contained an EcoRI site with the sequence:

5'-CGTGAATTCCAAGAATTTACAATCCTTGCT-3' (SEQ.ID.NO.: 102).

The 1.6 kb PCR fragment was digested with HindIII and EcoRI and cloned into HindIII-EcoRI site of pCMV expression vector. Nucleic acid (SEQ.ID.NO.: 103) and amino acid
10 (SEQ.ID.NO.: 104) sequences for human HB954 were thereafter determined and verified.

33. HG38 (GenBank Accession Number: AF062006)

The cDNA for human HG38 was generated and cloned into pCMV expression vector as follows: PCR was performed using brain cDNA as template and rTth polymerase (Perkin Elmer) with the buffer system provided by the manufacturer, 0.25 μ M of each primer, and 0.2 mM
15 of each 4 nucleotides. The cycle condition was 30 cycles of 94°C for 1 min, 56°C for 1 min and 72°C for 1 min and 30 sec. Two PCR reactions were performed to separately obtain the 5' and 3' fragment. For the 5' fragment, the 5' PCR primer contained an HindIII site with the sequence:

5'-CCCAAGCTTCGGGCACCATGGACACCTCCC-3' (SEQ.ID.NO.: 259)

and the 3' primer contained a BamHI site with the sequence:

20 5'-ACAGGATCCAAATGCACAGCACTGGTAAGC-3' (SEQ.ID.NO.: 260).

This 5' 1.5 kb PCR fragment was digested with HindIII and BamHI and cloned into an HindIII-BamHI site of pCMV. For the 3' fragment, the 5' PCR primer was kinased with the sequence:

5'-CTATAACTGGGTACATGGTTTAAC-3' (SEQ.ID.NO. 261)

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and the 3' primer contained an EcoRI site with the sequence:

5'-TTTGAATTCACATATTAATTAGAGACATGG-3' (SEQ.ID.NO.: 262).

The 1.4 kb 3' PCR fragment was digested with EcoRI and subcloned into a blunt-EcoRI site of pCMV vector. The 5' and 3' fragments were then ligated together through a common EcoRV site
5 to generate the full length cDNA clone. Nucleic acid (SEQ.ID.NO.: 263) and amino acid (SEQ.ID.NO.: 264) sequences for human HG38 were thereafter determined and verified.

34. HM74 (GenBank Accession Number: D10923)

The cDNA for human HM74 was generated and cloned into pCMV expression vector as follows: PCR was performed using either genomic DNA or thymus cDNA (pooled) as
10 template and rTth polymerase (Perkin Elmer) with the buffer system provided by the manufacturer, 0.25 μ M of each primer, and 0.2 mM of each of the 4 nucleotides. The cycle condition was 30 cycles of: 94°C for 1 min; 65°C for 1min; and 72°C for 1 min and 20 sec. The
5' PCR primer contained an EcoRI site with the sequence:

5'-GGAGAATTCAGTAGGCGAGGCGCTCCATC-3' (SEQ.ID.NO.: 105)

15 and the 3' primer was kinased with the sequence:

5'-GGAGGATCCAGGAAACCTTAGGCCGAGTCC-3' (SEQ.ID.NO.:106).

The 1.3 kb PCR fragment was digested with EcoRI and cloned into EcoRI-SmaI site of pCMV expression vector. Clones sequenced revealed a potential polymorphism involving a
N94K change. Aside from this difference, nucleic acid (SEQ.ID.NO.: 107) and amino acid
20 (SEQ.ID.NO.: 108) sequences for human HM74 were thereafter determined and verified.

35. MIG (GenBank Accession Numbers: AFO44600 and AFO44601)

The cDNA for human MIG was generated and cloned into pCMV expression vector as follows: PCR was performed using genomic DNA as template and TaqPlus Precision

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polymerase (Stratagene) for first round PCR or pfu polymerase (Stratagene) for second round PCR with the buffer system provided by the manufacturer, 0.25 μ M of each primer, and 0.2 mM (TaqPlus Precision) or 0.5 mM (pfu) of each of the 4 nucleotides. When pfu was used, 10% DMSO was included in the buffer. The cycle condition was 30 cycles of: 94°C for 1 min; 65°C
5 for 1 min; and 72 °C for: (a) 1 min for first round PCR; and (b) 2 min for second round PCR. Because there is an intron in the coding region, two sets of primers were separately used to generate overlapping 5' and 3' fragments. The 5' fragment PCR primers were:

5'-ACCATGGCTTGCAATGGCAGTGCGGCCAGGGGGCACT-3' (external sense)
(SEQ.ID.NO.: 109)

10 and

5'-CGACCAGGACAAACAGCATCTTGGTCACTTGTCTCCGGC-3' (internal antisense)
(SEQ.ID.NO.: 110).

The 3' fragment PCR primers were:

5'-GACCAAGATGCTGTTTGTCTCGTGGTGGTGGTGGCAT-3' (internal sense)
15 (SEQ.ID.NO.: 111) and

5'-CGGAATTCAGGATGGATCGGTCTCTTGCTGCGCCT-3' (external antisense with an
EcoRI site) (SEQ.ID.NO.: 112).

The 5' and 3' fragments were ligated together by using the first round PCR as template and the
kinased external sense primer and external antisense primer to perform second round PCR. The
20 1.2 kb PCR fragment was digested with EcoRI and cloned into the blunt-EcoRI site of pCMV
expression vector. Nucleic acid (SEQ.ID.NO.: 113) and amino acid (SEQ.ID.NO.: 114)
sequences for human MIG were thereafter determined and verified.

36. OGR1 (GenBank Accession Number: U48405)

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The cDNA for human OGR1 was generated and cloned into pCMV expression vector as follows: PCR was performed using genomic DNA as template and rTth polymerase (Perkin Elmer) with the buffer system provided by the manufacturer, 0.25 μ M of each primer, and 0.2 mM of each of the 4 nucleotides. The cycle condition was 30 cycles of: 94°C for 1 min; 65°C for 1min; and 72°C for 1 min and 20 sec. The 5' PCR primer was kinased with the sequence: 5'-GGAAGCTTCAGGCCCAAAGATGGGGAACAT-3' (SEQ.ID.NO.: 115); and the 3' primer contained a BamHI site with the sequence: 5'-GTGGATCCACCCGCGGAGGACCCAGGCTAG -3' (SEQ.ID.NO.: 116). The 1.1 kb PCR fragment was digested with BamHI and cloned into the EcoRV-BamHI site of pCMV expression vector. Nucleic acid (SEQ.ID.NO.: 117) and amino acid (SEQ.ID.NO.: 118) sequences for human OGR1 were thereafter determined and verified.

37. Serotonin 5HT_{2A}

The cDNA encoding endogenous human 5HT_{2A} receptor was obtained by RT-PCR using human brain poly-A⁺ RNA; a 5' primer from the 5' untranslated region with an Xho I restriction site:

5'-GACCTCGAGTCCTTCTACACCTCATC-3' (SEQ.ID.NO: 119)

and a 3' primer from the 3' untranslated region containing an Xba I site:

5'-TGCTCTAGATTCCAGATAGGTGAAAACCTTG-3' (SEQ.ID.NO: 120)

PCR was performed using either TaqPlus™ precision polymerase (Stratagene) or rTth™ polymerase (Perkin Elmer) with the buffer system provided by the manufacturers, 0.25 μ M of each primer, and 0.2 mM of each of the 4 nucleotides. The cycle condition was 30 cycles of: 94°C for 1 min; 57°C for 1min; and 72°C for 2 min. The 1.5 kb PCR fragment was digested with Xba I and subcloned into Eco RV-Xba I site of pBluescript. The resulting cDNA clones were fully

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sequenced and found to encode two amino acid changes from the published sequences. The first one was a T25N mutation in the N-terminal extracellular domain; the second is an H452Y mutation. Because cDNA clones derived from two independent PCR reactions using Taq polymerase from two different commercial sources (TaqPlus™ from Stratagene and rTth™ Perkin Elmer) contained the same two mutations, these mutations are likely to represent sequence polymorphisms rather than PCR errors. With these exceptions, the nucleic acid (SEQ.ID.NO.: 121) and amino acid (SEQ.ID.NO.: 122) sequences for human 5HT_{2A} were thereafter determined and verified.

38. Serotonin 5HT_{2C}

10 The cDNA encoding endogenous human 5HT_{2C} receptor was obtained from human brain poly-A⁺ RNA by RT-PCR. The 5' and 3' primers were derived from the 5' and 3' untranslated regions and contained the following sequences:

5'-GACCTCGAGGTTGCTTAAGACTGAAGC-3' (SEQ.ID.NO.: 123)

5'-ATTTCTAGACATATGTAGCTTGTACCG-3' (SEQ.ID.NO.: 124)

15 Nucleic acid (SEQ.ID.NO.: 125) and amino acid (SEQ.ID.NO.: 126) sequences for human 5HT_{2C} were thereafter determined and verified.

39. V28 (GenBank Accession Number: U20350)

 The cDNA for human V28 was generated and cloned into pCMV expression vector as follows: PCR was performed using brain cDNA as template and rTth polymerase (Perkin Elmer) with the buffer system provided by the manufacturer, 0.25 μM of each primer, and 0.2 mM of each of the 4 nucleotides. The cycle condition was 30 cycles of: 94°C for 1 min; 65°C for 1 min; and 72°C for 1 min and 20 sec. The 5' PCR primer contained a HindIII site with the sequence:

20 5'-GGTAAGCTTGGCAGTCCACGCCAGGCCTTC-3' (SEQ.ID.NO.: 127)

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and the 3' primer contained an EcoRI site with the sequence:

5'-TCCGAATTCTCTGTAGACACAAGGCTTTGG-3' (SEQ.ID.NO.: 128)

The 1.1 kb PCR fragment was digested with HindIII and EcoRI and cloned into HindIII-EcoRI site of pCMV expression vector. Nucleic acid (SEQ.ID.NO.: 129) and amino acid (SEQ.ID.NO.:

5 130) sequences for human V28 were thereafter determined and verified.

Example 2

PREPARATION OF NON-ENDOGENOUS HUMAN GPCRS

1. Site-Directed Mutagenesis

Mutagenesis based upon the Human GPCR Proline Marker approach disclosed herein was performed on the foregoing endogenous human GPCRs using Transformer Site-Directed Mutagenesis Kit (Clontech) according to the manufacturer instructions. For this mutagenesis approach, a Mutation Probe and a Selection Marker Probe (unless otherwise indicated, the probe of SEQ.ID.NO.: 132 was the same throughout) were utilized, and the sequences of these for the specified sequences are listed below in Table B (the parenthetical number is the SEQ. ID.NO.). For convenience, the codon mutation incorporated into the human GPCR is also noted, in standard form:

Table B

Receptor Identifier (Codon Mutation)	Mutation Probe Sequence (5'-3') (SEQ.ID.NO.)	Selection Marker Probe Sequence (5'-3') (SEQ.ID.NO.)
20 GPR1 (F245K)	GATCTCCAGTAGGCAT <u>AAGT</u> GGACAATTCTGG (131)	CTCCTTCGGTCCTCCTATCGT TGTCAGAAG (132)
GPR4 (K223A)	AGAAGGCCAAGATC <u>GCGCGG</u> CTGGCCCTCA (133)	CTCCTTCGGTCCTCCTATCGT TGTCAGAAGT
25 GPR5 (V224K)	CGGCGCCACCGCACG <u>AAAAA</u> GTCATCTTC	CTCCTTCGGTCCTCCTATCGT TGTCAGAAGT

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	(134)	
GPR7 (T250K)	GCCAAGAAGCGGGTGAAGTT CCTGGTGGTGGCA (135)	CTCCTTCGGTCCTCCTATCGT TGTCAGAAAGT
GPR8 (T259K)	CAGGCGGAAGGTGAAAGTCC TGGTCCTCGT (136)	CTCCTTCGGTCCTCCTATCGT TGTCAGAAAGT
30 GPR9 (M254K)	CGGCGCCTGCGGGCCAGCG GCTGGTGGTGGT (137)	CTCCTTCGGTCCTCCTATCGT TGTCAGAAAGT
GPR9-6 (L241K)	CCAAGCACAAAGCCAAGAAA GTGACCATCAC (138)	CTCCTTCGGTCCTCCTATCGT TGTCAGAAAGT
35 GPR10 (F276K)	GCGCCGGCGCACCAAAATGCT TGCTGGTGGT (139)	CTCCTTCGGTCCTCCTATCGT TGTCAGAAAGT
GPR15 (I240K)	CAAAAAGCTGAAGAAATCTA AGAAGATCATCTTATTGTCG (140)	CTCCTTCGGTCCTCCTATCGT TGTCAGAAAGT
GPR17 (V234K)	CAAGACCAAGGCCAAAACGCA TGATCGCCAT (141)	CTCCTTCGGTCCTCCTATCGT TGTCAGAAAGT
40 GPR18 (I231K)	GTCAAGGAGAAGTCCAAAAG GATCATCATC (142)	CTCCTTCGGTCCTCCTATCGT TGTCAGAAAGT
GPR20 (M240K)	CGCCGCGTGCGGGCCAGCA GCTCCTGCTC (143)	CTCCTTCGGTCCTCCTATCGT TGTCAGAAAGT
45 GPR21 (A251K)	CCTGATAAGCGCTATAAAAT GGTCCTGTTTCGA (144)	CTCCTTCGGTCCTCCTATCGT TGTCAGAAAGT
GPR22 (F312K)	GAAAGACAAAAGAGAGTCA AGAGGATGTCTTTATTG (145)	CTCCTTCGGTCCTCCTATCGT TGTCAGAAAGT
GPR24 (T304K)	CGGAGAAAGAGGGTGAAAC GCACAGCCATCGCC (146)	CTCCTTCGGTCCTCCTATCGT TGTCAGAAAGT
50 GPR30 (L258K)	alternate approach; <i>see</i> below	alternate approach; <i>see</i> below
GPR31 (Q221K)	AAGCTTCAGCGGGCCAAAGC ACTGGTCACC (147)	CTCCTTCGGTCCTCCTATCGT TGTCAGAAAGT
55 GPR32 (K255A)	CATGCCAACCGGCCCCGCGAG GCTGCTGCTGGT (279)	ACCAGCAGCAGCCTCGCGGG CCGGTTGGCATG (280)
GPR40 (A223K)	CGGAAGCTGCGGGCCAAATG GGTGGCCGGC (265)	CTCCTTCGGTCCTCCTATCGT TGTCAGAAAGT
GPR41	CAGAGGAGGGTGAGGGGGCT GTTGGCG	CTCCTTCGGTCCTCCTATCGT TGTCAGAAAGT

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(A223K)	(266)	
GPR43 (V221K)	GGCGGCGCCGAGCC <u>AAGGGG</u> CTGGCTGTGG (267)	CTCCTTCGGTCCTCCTATCGT TGTCAGAAAGT
APJ (L247K)	alternate approach; <i>see below</i>	alternate approach; <i>see below</i>
BLR1 (V258K)	CAGCGGCAGAAGGCC <u>AAAA</u> GGGTGGCCATC (148)	CTCCTTCGGTCCTCCTATCGT TGTCAGAAAGT
CEPR (L258K)	CGGCAGAAGGCG <u>AAGCGCAT</u> GATCCTCGCG (149)	CTCCTTCGGTCCTCCTATCGT TGTCAGAAAGT
10 EBI1 (I262K)	GAGCGCAACAAGGCC <u>AAAA</u> AGGTGATCATC (150)	CTCCTTCGGTCCTCCTATCGT TGTCAGAAAGT
EBI2 (L243K)	GGTGTAACAAAAAGGCT <u>AA</u> <u>AAACACAATTATTC</u> TATT (151)	CTCCTTCGGTCCTCCTATCGT TGTCAGAAAGT
ETBR-LP2 (N358K)	GAGAGCCAGCTCA <u>AAGAGCAC</u> CGTGGTG (152)	CTCCTTCGGTCCTCCTATCGT TGTCAGAAAGT
15 GHSR (V262K)	CCACAAGCAAACCA <u>AAGAAAA</u> TGCTGGCTGT (153)	CTCCTTCGGTCCTCCTATCGT TGTCAGAAAGT
GPCR-CNS (N491K)	CTAGAGAGTCAGATG <u>AAGTG</u> TACAGTAGTGGCAC (155)	CTCCTTCGGTCCTCCTATCGT TGTCAGAAAGT
20 GPR-NGA (I275K)	CGGACAAAAGTGAA <u>AACTAA</u> <u>AAAGATGTTCTC</u> TATT (156)	CTCCTTCGGTCCTCCTATCGT TGTCAGAAAGT
H9a and H9b (F236K)	GCTGAGGTTTCGCAAT <u>AAACT</u> AACCATGTTTGTG (157)	CTCCTTCGGTCCTCCTATCGT TGTCAGAAAGT
HB954 (H265K)	GGGAGGCCGAGCTG <u>AAAGCC</u> ACCCTGCTC (158)	CTCCTTCGGTCCTCCTATCGT TGTCAGAAAGT
25 HG38 (V765K)	GGGACTGCTCTATG <u>AAAAAA</u> CACATTGCCCTG (268)	CATCAAGTGTATCATGTGCC AAGTACGCCC (154)
HM74 (I230K)	CAAGATCAAGAGAGCC <u>AAAA</u> CCTTCATCATG (159)	CTCCTTCGGTCCTCCTATCGT TGTCAGAAAGT
30 MIG (T273K)	CCGGAGACAAGTG <u>AAGAAG</u> ATGCTGTTTGTG (160)	CTCCTTCGGTCCTCCTATCGT TGTCAGAAAGT
OGR1 (Q227K)	GCAAGGACCAGATCA <u>AAGCGG</u> CTGGTGCTCA (161)	CTCCTTCGGTCCTCCTATCGT TGTCAGAAAGT
Serotonin 5HT _{2A} (C322K)	alternate approach; <i>see below</i>	alternate approach; <i>see below</i>
35 Serotonin 5HT _{2C} (S310K)	alternate approach; <i>see below</i>	alternate approach; <i>see below</i>

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V28 (I230K)	CAAGAAAGCCAAAGCC <u>AAG</u> AAACTGATCCTTCTG (162)	CTCCTTCGGTCCTCCTATCGT TGTCAGAAAGT
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The non-endogenous human GPCRs were then sequenced and the derived and verified nucleic acid and amino acid sequences are listed in the accompanying "Sequence Listing" appendix.

5 to this patent document, as summarized in Table C below:

Table C

	Mutated GPCR	Nucleic Acid Sequence Listing	Amino Acid Sequence Listing
	GPR1 (F245K)	SEQ.ID.NO.: 163	SEQ.ID.NO.: 164
10	GPR4 (K223A)	SEQ.ID.NO.: 165	SEQ.ID.NO.: 166
	GPR5 (V224K)	SEQ.ID.NO.: 167	SEQ.ID.NO.: 168
15	GPR7 (T250K)	SEQ.ID.NO.: 169	SEQ.ID.NO.: 170
	GPR8 (T259K)	SEQ.ID.NO.: 171	SEQ.ID.NO.: 172
	GPR9 (M254K)	SEQ.ID.NO.: 173	SEQ.ID.NO.: 174
20	GPR9-6 (L241K)	SEQ.ID.NO.: 175	SEQ.ID.NO.: 176
	GPR10 (F276K)	SEQ.ID.NO.: 177	SEQ.ID.NO.: 178
25	GPR15 (I240K)	SEQ.ID.NO.: 179	SEQ.ID.NO.: 180
	GPR17 (V234K)	SEQ.ID.NO.: 181	SEQ.ID.NO.: 182
	GPR18 (I231K)	SEQ.ID.NO.: 183	SEQ.ID.NO.: 184
30	GPR20 (M240K)	SEQ.ID.NO.: 185	SEQ.ID.NO.: 186
	GPR21 (A251K)	SEQ.ID.NO.: 187	SEQ.ID.NO.: 188
35	GPR22 (F312K)	SEQ.ID.NO.: 189	SEQ.ID.NO.: 190
	GPR24 (T304K)	SEQ.ID.NO.: 191	SEQ.ID.NO.: 192
	GPR30	SEQ.ID.NO.: 193	SEQ.ID.NO.: 194

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	(L258K)		
	GPR31 (Q221K)	SEQ.ID.NO.: 195	SEQ.ID.NO.: 196
	GPR32 (K255A)	SEQ.ID.NO.: 269	SEQ.ID.NO.: 270
5	GPR40 (A223K)	SEQ.ID.NO.: 271	SEQ.ID.NO.: 272
	GPR41 (A223K)	SEQ.ID.NO.: 273	SEQ.ID.NO.: 274
10	GPR43 (V221K)	SEQ.ID.NO.: 275	SEQ.ID.NO.: 276
	APJ (L247K)	SEQ.ID.NO.: 197	SEQ.ID.NO.: 198
	BLR1 (V258K)	SEQ.ID.NO.: 199	SEQ.ID.NO.: 200
15	CEPR (L258K)	SEQ.ID.NO.: 201	SEQ.ID.NO.: 202
	EBI1 (I262K)	SEQ.ID.NO.: 203	SEQ.ID.NO.: 204
20	EBI2 (L243K)	SEQ.ID.NO.: 205	SEQ.ID.NO.: 206
	ETBR-LP2 (N358K)	SEQ.ID.NO.: 207	SEQ.ID.NO.: 208
	GHSR (V262K)	SEQ.ID.NO.: 209	SEQ.ID.NO.: 210
25	GPCR-CNS (N491K)	SEQ.ID.NO.: 211	SEQ.ID.NO.: 212
	GPR-NGA (I275K)	SEQ.ID.NO.: 213	SEQ.ID.NO.: 214
30	H9a (F236K)	SEQ.ID.NO.: 215	SEQ.ID.NO.: 216
	H9b (F236K)	SEQ.ID.NO.: 217	SEQ.ID.NO.: 218
	HB954 (H265K)	SEQ.ID.NO.: 219	SEQ.ID.NO.: 220
35	HG38 (V765K)	SEQ.ID.NO.: 277	SEQ.ID.NO.: 278
	HM74 (I230K)	SEQ.ID.NO.: 221	SEQ.ID.NO.: 222
40	MIG (T273K)	SEQ.ID.NO.: 223	SEQ.ID.NO.: 224
	OGR1 (Q227K)	SEQ.ID.NO.: 225	SEQ.ID.NO.: 226
	Serotonin 5HT _{2A} (C322K)	SEQ.ID.NO.: 227	SEQ.ID.NO.: 228
45	Serotonin 5HT _{2C} (S310K)	SEQ.ID.NO.: 229	SEQ.ID.NO.: 230
	V28 (I230K)	SEQ.ID.NO.: 231	SEQ.ID.NO.: 232

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2. **Alternate Mutation Approaches for Employment of the Proline Marker Algorithm: APJ; Serotonin 5HT_{2A}; Serotonin 5HT_{2C}; and GPR30**

Although the above site-directed mutagenesis approach is particularly preferred, other approaches can be utilized to create such mutations; those skilled in the art are readily credited with selecting approaches to mutating a GPCR that fits within the particular needs of the artisan.

a. **APJ**

Preparation of the non-endogenous, human APJ receptor was accomplished by mutating L247K. Two oligonucleotides containing this mutation were synthesized:

5'-GGCTTAAGAGCATCATCGTGGTGCTGGTG-3' (SEQ.ID.NO.: 233)

10 5'-GTCACCACCAGCACCACGATGATGCTCTTAAGCC-3' (SEQ.ID.NO.: 234)

The two oligonucleotides were annealed and used to replace the NaeI-BstEII fragment of human, endogenous APJ to generate the non-endogenous, version of human APJ.

b. **Serotonin 5HT_{2A}**

cDNA containing the point mutation C322K was constructed by utilizing the restriction enzyme site Sph I which encompasses amino acid 322. A primer containing the C322K mutation:

5'-CAAAGAAAGTACTGGGCATCGTCTTCTTCCT-3' (SEQ.ID.NO: 235)

was used along with the primer from the 3' untranslated region of the receptor:

5'-TGCTCTAGATTCCAGATAGGTGAAAA CTTG-3' (SEQ.ID.NO.: 236)

to perform PCR (under the conditions described above). The resulting PCR fragment was then used to replace the 3' end of endogenous 5HT_{2A} cDNA through the T4 polymerase blunted Sph I site.

c. **Serotonin 5HT_{2C}**

The cDNA containing a S310K mutation was constructed by replacing the Sty I restriction fragment containing amino acid 310 with synthetic double stranded oligonucleotides that encode

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the desired mutation. The sense strand sequence utilized had the following sequence:

5'-CTAGGGGCACCATGCAGGCTATCAACAATGAAAGAAAAGCTAAGAAAGTC-3'
(SEQ. ID.NO.: 237)

and the antisense strand sequence utilized had the following sequence:

5'-CAAGGACTTTCTTAGCTTTTCTTTCATTGTTGATAGCCTGCATGGTGCCC-3' (SEQ.
ID. NO.: 238)

d. GPR30

Prior to generating non-endogenous GPR30, several independent pCR2.1/GPR30 isolates were sequenced in their entirety in order to identify clones with no PCR-generated mutations. A clone having no mutations was digested with EcoRI and the endogenous GPR30 cDNA fragment was transferred into the CMV-driven expression plasmid pCI-neo (Promega), by digesting pCI-Neo with EcoRI and subcloning the EcoRI-liberated GPR30 fragment from pCR2.1/GPR30, to generate pCI/GPR30. Thereafter, the leucine at codon 258 was mutated to a lysine using a Quick-Change™ Site-Directed Mutagenesis Kit (Stratagene, #200518), according to manufacturer's instructions, and the following primers:

5'-CGGCGGCAGAAGGCGAAACGCATGATCCTCGCGGT-3' (SEQ.ID.NO.: 239) and
5'-ACCGCGAGGATCATGCGTTTCGCCTTCTGC CGCCG-3' (SEQ.ID.NO.: 240)

Example 3

Receptor (Endogenous and Mutated) Expression

Although a variety of cells are available to the art for the expression of proteins, it is most preferred that mammalian cells be utilized. The primary reason for this is predicated upon practicalities, *i.e.*, utilization of, *e.g.*, yeast cells for the expression of a GPCR, while possible,

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introduces into the protocol a non-mammalian cell which may not (indeed, in the case of yeast, does not) include the receptor-coupling, genetic-mechanism and secretory pathways that have evolved for mammalian systems – thus, results obtained in non-mammalian cells, while of potential use, are not as preferred as that obtained from mammalian cells. Of the mammalian cells, COS-7, 293 and 293T cells are particularly preferred, although the specific mammalian cell utilized can be predicated upon the particular needs of the artisan.

Unless otherwise noted herein, the following protocol was utilized for the expression of the endogenous and non-endogenous human GPCRs. Table D lists the mammalian cell and number utilized (per 150mm plate) for GPCR expression.

10

Table D

15

20

Receptor Name (Endogenous or Non-Endogenous)	Mammalian Cell (Number Utilized)
GPR17	293 (2×10^6)
GPR30	293 (4×10^6)
APJ	COS-7 (5×10^6)
ETBR-LP2	293 (1×10^7)
	293T (1×10^7)
GHSR	293 (1×10^7)
	293T (1×10^7)
MIG	293 (1×10^7)
Serotonin 5HT _{2A}	293T (1×10^7)
Serotonin 5HT _{2c}	293T (1×10^7)

On day one, mammalian cells were plated out. On day two, two reaction tubes were prepared (the proportions to follow for each tube are per plate): tube A was prepared by mixing 20µg DNA (*e.g.*, pCMV vector, pCMV vector with endogenous receptor cDNA, and pCMV vector with non-endogenous receptor cDNA.) in 1.2ml serum free DMEM (Irvine Scientific,

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Irvine, CA); tube B was prepared by mixing 120 μ l lipofectamine (Gibco BRL) in 1.2ml serum free DMEM. Tubes A and B were then admixed by inversions (several times), followed by incubation at room temperature for 30-45min. The admixture is referred to as the "transfection mixture". Plated cells were washed with 1XPBS, followed by addition of 10ml serum free
5 DMEM. 2.4ml of the transfection mixture was then added to the cells, followed by incubation for 4hrs at 37°C/5% CO₂. The transfection mixture was then removed by aspiration, followed by the addition of 25ml of DMEM/10% Fetal Bovine Serum. Cells were then incubated at 37°C/5% CO₂. After 72hr incubation, cells were then harvested and utilized for analysis.

1. Gi-Coupled Receptors: Co-Transfection with Gs-Coupled Receptors

10 In the case of GPR30, it has been determined that this receptor couples the G protein Gi. Gi is known to inhibit the enzyme adenylyl cyclase, which is necessary for catalyzing the conversion of ATP to cAMP. Thus, a non-endogenous, constitutively activated form of GPR30 would be expected to be associated with decreased levels of cAMP. Assay confirmation of a non-endogenous, constitutively activated form of GPR30 directly via measurement of decreasing levels
15 of cAMP, while viable, can be preferably measured by cooperative use of a Gs-coupled receptor. For example, a receptor that is Gs-coupled will stimulate adenylyl cyclase, and thus will be associated with an increase in cAMP. The assignee of the present application has discovered that the orphan receptor GPR6 is an endogenous, constitutively activated GPCR. GPR6 couples to the Gs protein. Thus when co-transfected, one can readily verify that a putative GPR30-mutation
20 leads to constitutive activation thereof: *i.e.*, an endogenous, constitutively activated GPR6/endogenous, non-constitutively activated GPR30 cell will evidence an elevated level of cAMP when compared with an endogenous, constitutively active GPR6/non-endogenous, constitutively activated GPR30 (the latter evidencing a comparatively lower level of cAMP).

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Assays that detect cAMP can be utilized to determine if a candidate compound is *e.g.*, an inverse agonist to a Gs-associated receptor (*i.e.*, such a compound would decrease the levels of cAMP) or a Gi-associated receptor (or a Go-associated receptor) (*i.e.*, such a candidate compound would increase the levels of cAMP). A variety of approaches known in the art for measuring cAMP can be utilized; a preferred approach relies upon the use of anti-cAMP antibodies. Another approach, and most preferred, utilizes a whole cell second messenger reporter system assay. Promoters on genes drive the expression of the proteins that a particular gene encodes. Cyclic AMP drives gene expression by promoting the binding of a cAMP-responsive DNA binding protein or transcription factor (CREB) which then binds to the promoter at specific sites called cAMP response elements and drives the expression of the gene. Reporter systems can be constructed which have a promoter containing multiple cAMP response elements before the reporter gene, *e.g.*, β -galactosidase or luciferase. Thus, an activated receptor such as GPR6 causes the accumulation of cAMP which then activates the gene and expression of the reporter protein. Most preferably, 293 cells are co-transfected with GPR6 (or another Gs-linked receptor) and GPR30 (or another Gi-linked receptor) plasmids, preferably in a 1:1 ratio, most preferably in a 1:4 ratio. Because GPR6 is an endogenous, constitutively active receptor that stimulates the production of cAMP, GPR6 strongly activates the reporter gene and its expression. The reporter protein such as β -galactosidase or luciferase can then be detected using standard biochemical assays (Chen et al. 1995). Co-transfection of endogenous, constitutively active GPR6 with endogenous, non-constitutively active GPR30 evidences an increase in the luciferase reporter protein. Conversely, co-transfection of endogenous, constitutively active GPR6 with non-endogenous, constitutively active GPR30 evidences a drastic decrease in expression of luciferase. Several reporter plasmids are known and available in the art for measuring a second messenger assay. It is considered well within the

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skilled artisan to determine an appropriate reporter plasmid for a particular gene expression based primarily upon the particular need of the artisan. Although a variety of cells are available for expression, mammalian cells are most preferred, and of these types, 293 cells are most preferred. 293 cells were transfected with the reporter plasmid pCRE-Luc/GPR6 and non-endogenous, 5 constitutively activated GPR30 using a Mammalian Transfection™ Kit (Stratagene, #200285) CaPO₄ precipitation protocol according to the manufacturer's instructions (*see*, 28 Genomics 347 (1995) for the published endogenous GPR6 sequence). The precipitate contained 400ng reporter, 80ng CMV-expression plasmid (having a 1:4 GPR6 to endogenous GPR30 or non-endogenous GPR30 ratio) and 20ng CMV-SEAP (a transfection control plasmid encoding secreted alkaline 10 phosphatase). 50% of the precipitate was split into 3 wells of a 96-well tissue culture dish (containing 4X10⁴ cells/well); the remaining 50% was discarded. The following morning, the media was changed. 48 hr after the start of the transfection, cells were lysed and examined for luciferase activity using a Lucite™ Kit (Packard, Cat. # 6016911) and Trilux 1450 Microbeta™ liquid scintillation and luminescence counter (Wallac) as per the vendor's instructions. The data 15 were analyzed using GraphPad Prism 2.0a (GraphPad Software Inc.).

With respect to GPR17, which has also been determined to be Gi-linked, a modification of the foregoing approach was utilized, based upon, *inter alia*, use of another Gs-linked endogenous receptor, GPR3 (*see* 23 Genomics 609 (1994) and 24 Genomics 391 (1994)). Most preferably, 293 cells are utilized. These cells were plated-out on 96 well plates at a density of 2 20 x 10⁴ cells per well and were transfected using Lipofectamine Reagent (BRL) the following day according to manufacturer instructions. A DNA/lipid mixture was prepared for each 6-well transfection as follows: 260ng of plasmid DNA in 100μl of DMEM were gently mixed with 2μl of lipid in 100μl of DMEM (the 260ng of plasmid DNA consisted of 200ng of a 8xCRE-Luc

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reporter plasmid (*see below*), 50ng of pCMV comprising endogenous receptor or non-endogenous receptor or pCMV alone, and 10ng of a GPRS expression plasmid (GPRS in pcDNA3 (Invitrogen)). The 8XCRE-Luc reporter plasmid was prepared as follows: vector SRIF- β -gal was obtained by cloning the rat somatostatin promoter (-71/+51) at BglV-HindIII site in the p β gal-Basic Vector (Clontech). Eight (8) copies of cAMP response element were obtained by PCR from
5 Basic Vector (Clontech). Eight (8) copies of cAMP response element were obtained by PCR from an adenovirus template AdpCF126CCRE8 (*see* 7 Human Gene Therapy 1883 (1996)) and cloned into the SRIF- β -gal vector at the Kpn-BglV site, resulting in the 8xCRE- β -gal reporter vector. The 8xCRE-Luc reporter plasmid was generated by replacing the beta-galactosidase gene in the 8xCRE- β -gal reporter vector with the luciferase gene obtained from the pGL3-basic vector
10 (Promega) at the HindIII-BamHI site. Following 30min. incubation at room temperature, the DNA/lipid mixture was diluted with 400 μ l of DMEM and 100 μ l of the diluted mixture was added to each well. 100 μ l of DMEM with 10% FCS were added to each well after a 4hr incubation in a cell culture incubator. The next morning the transfected cells were changed with 200 μ l/well of DMEM with 10% FCS. Eight (8) hours later, the wells were changed to 100 μ l /well of DMEM
15 without phenol red, after one wash with PBS. Luciferase activity were measured the next day using the LucLite™ reporter gene assay kit (Packard) following manufacturer instructions and read on a 1450 MicroBeta™ scintillation and luminescence counter (Wallac).

Figure 4 evidences that constitutively active GPR30 inhibits GPR6-mediated activation of CRE-Luc reporter in 293 cells. Luciferase was measured at about 4.1 relative
20 light units in the expression vector pCMV. Endogenous GPR30 expressed luciferase at about 8.5 relative light units, whereas the non-endogenous, constitutively active GPR30 (L258K), expressed luciferase at about 3.8 and 3.1 relative light units, respectively. Co-transfection of endogenous GPR6 with endogenous GPR30, at a 1:4 ratio, drastically increased luciferase

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expression to about 104.1 relative light units. Co-transfection of endogenous GPR6 with non-endogenous GPR30 (L258K), at the same ratio, drastically decreased the expression, which is evident at about 18.2 and 29.5 relative light units, respectively. Similar results were observed with respect to GPR17 with respect to co-transfection with GPR3, as set forth in

5 Figure 5.

Example 3

ASSAYS FOR DETERMINATION OF CONSTITUTIVE ACTIVITY OF NON-ENDOGENOUS GPCRS

A. Membrane Binding Assays

10 1. [³⁵S]GTP γ S Assay

When a G protein-coupled receptor is in its active state, either as a result of ligand binding or constitutive activation, the receptor couples to a G protein and stimulates the release of GDP and subsequent binding of GTP to the G protein. The alpha subunit of the G protein-receptor complex acts as a GTPase and slowly hydrolyzes the GTP to GDP, at which point the receptor normally is deactivated. Constitutively activated receptors continue to exchange GDP for GTP. 15 The non-hydrolyzable GTP analog, [³⁵S]GTP γ S, can be utilized to demonstrate enhanced binding of [³⁵S]GTP γ S to membranes expressing constitutively activated receptors. The advantage of using [³⁵S]GTP γ S binding to measure constitutive activation is that: (a) it is generically applicable to all G protein-coupled receptors; (b) it is proximal at the membrane surface making it less likely 20 to pick-up molecules which affect the intracellular cascade.

The assay utilizes the ability of G protein coupled receptors to stimulate [³⁵S]GTP γ S binding to membranes expressing the relevant receptors. The assay can, therefore, be used in the direct identification method to screen candidate compounds to known, orphan and constitutively activated G protein-coupled receptors. The assay is generic and has application

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to drug discovery at all G protein-coupled receptors.

The [^{35}S]GTP γ S assay was incubated in 20 mM HEPES and between 1 and about 20mM MgCl_2 (this amount can be adjusted for optimization of results, although 20mM is preferred) pH 7.4, binding buffer with between about 0.3 and about 1.2 nM [^{35}S]GTP γ S (this amount can be adjusted
5 for optimization of results, although 1.2 is preferred) and 12.5 to 75 μg membrane protein (*e.g.* COS-7 cells expressing the receptor; this amount can be adjusted for optimization, although 75 μg is preferred) and 1 μM GDP (this amount can be changed for optimization) for 1 hour. Wheatgerm agglutinin beads (25 μl ; Amersham) were then added and the mixture was incubated for another 30 minutes at room temperature. The tubes were then centrifuged at 1500 x g for 5
10 minutes at room temperature and then counted in a scintillation counter.

A less costly but equally applicable alternative has been identified which also meets the needs of large scale screening. Flash platesTM and WallacTM scintistrips may be utilized to format a high throughput [^{35}S]GTP γ S binding assay. Furthermore, using this technique, the assay can be utilized for known GPCRs to simultaneously monitor tritiated ligand binding to the receptor at the
15 same time as monitoring the efficacy via [^{35}S]GTP γ S binding. This is possible because the Wallac beta counter can switch energy windows to look at both tritium and ^{35}S -labeled probes. This assay may also be used to detect other types of membrane activation events resulting in receptor activation. For example, the assay may be used to monitor ^{32}P phosphorylation of a variety of receptors (both G protein coupled and tyrosine kinase receptors). When the membranes are
20 centrifuged to the bottom of the well, the bound [^{35}S]GTP γ S or the ^{32}P -phosphorylated receptor will activate the scintillant which is coated of the wells. Scinti[®] strips (Wallac) have been used to demonstrate this principle. In addition, the assay also has utility for measuring ligand binding to receptors using radioactively labeled ligands. In a similar manner, when the radiolabeled bound

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ligand is centrifuged to the bottom of the well, the scintistrip label comes into proximity with the radiolabeled ligand resulting in activation and detection.

Representative results of graph comparing Control (pCMV), Endogenous APJ and Non-Endogenous APJ, based upon the foregoing protocol, are set forth in Figure 6.

5 2. Adenylyl Cyclase

A Flash Plate™ Adenylyl Cyclase kit (New England Nuclear; Cat. No. SMP004A) designed for cell-based assays was modified for use with crude plasma membranes. The Flash Plate wells contain a scintillant coating which also contains a specific antibody recognizing cAMP. The cAMP generated in the wells was quantitated by a direct competition for binding of
10 radioactive cAMP tracer to the cAMP antibody. The following serves as a brief protocol for the measurement of changes in cAMP levels in membranes that express the receptors.

Transfected cells were harvested approximately three days after transfection. Membranes were prepared by homogenization of suspended cells in buffer containing 20mM HEPES, pH 7.4 and 10mM MgCl₂. Homogenization was performed on ice using a Brinkman Polytron™ for
15 approximately 10 seconds. The resulting homogenate was centrifuged at 49,000 X g for 15 minutes at 4°C. The resulting pellet was then resuspended in buffer containing 20mM HEPES, pH 7.4 and 0.1 mM EDTA, homogenized for 10 seconds, followed by centrifugation at 49,000 X g for 15 minutes at 4°C. The resulting pellet can be stored at -80°C until utilized. On the day of measurement, the membrane pellet was slowly thawed at room temperature, resuspended in buffer
20 containing 20mM HEPES, pH 7.4 and 10mM MgCl₂ (these amounts can be optimized, although the values listed herein are preferred), to yield a final protein concentration of 0.60mg/ml (the resuspended membranes were placed on ice until use).

cAMP standards and Detection Buffer (comprising 2 µCi of tracer [¹²⁵I] cAMP (100 µl) to

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11 ml Detection Buffer) were prepared and maintained in accordance with the manufacturer's instructions. Assay Buffer was prepared fresh for screening and contained 20mM HEPES, pH 7.4, 10mM MgCl₂, 20mM (Sigma), 0.1 units/ml creatine phosphokinase (Sigma), 50 μ M GTP (Sigma), and 0.2 mM ATP (Sigma); Assay Buffer can be stored on ice until utilized. The assay
5 was initiated by addition of 50ul of assay buffer followed by addition of 50ul of membrane suspension to the NEN Flash Plate. The resultant assay mixture is incubated for 60 minutes at room temperature followed by addition of 100ul of detection buffer. Plates are then incubated an additional 2-4 hours followed by counting in a Wallac MicroBeta scintillation counter. Values of cAMP/well are extrapolated from a standard cAMP curve which is contained within each assay
10 plate. The foregoing assay was utilized with respect to analysis of MIG.

B. Reporter-Based Assays

1. CREB Reporter Assay (Gs-associated receptors)

A method to detect Gs stimulation depends on the known property of the transcription factor CREB, which is activated in a cAMP-dependent manner. A PathDetect CREB trans-
15 Reporting System (Stratagene, Catalogue # 219010) was utilized to assay for Gs coupled activity in 293 or 293T cells. Cells were transfected with the plasmids components of this above system and the indicated expression plasmid encoding endogenous or mutant receptor using a Mammalian Transfection Kit (Stratagene, Catalogue #200285) according to the manufacturer's instructions. Briefly, 400 ng pFR-Luc (luciferase reporter plasmid containing
20 Gal4 recognition sequences), 40 ng pFA2-CREB (Gal4-CREB fusion protein containing the Gal4 DNA-binding domain), 80 ng CMV-receptor expression plasmid (comprising the receptor) and 20 ng CMV-SEAP (secreted alkaline phosphatase expression plasmid; alkaline phosphatase activity is measured in the media of transfected cells to control for variations in

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transfection efficiency between samples) were combined in a calcium phosphate precipitate as per the Kit's instructions. Half of the precipitate was equally distributed over 3 wells in a 96-well plate, kept on the cells overnight, and replaced with fresh medium the following morning. Forty-eight (48) hr after the start of the transfection, cells were treated and assayed for luciferase activity as set forth with respect to the GPR30 system, above. This assay was used with respect to GHSR.

2. AP1 reporter assay (Gq-associated receptors)

A method to detect Gq stimulation depends on the known property of Gq-dependent phospholipase C to cause the activation of genes containing AP1 elements in their promoter. A Pathdetect AP-1 cis-Reporting System (Stratagene, Catalogue # 219073) was utilized following the protocol set forth above with respect to the CREB reporter assay, except that the components of the calcium phosphate precipitate were 410 ng pAP1-Luc, 80 ng receptor expression plasmid, and 20 ng CMV-SEAP. This assay was used with respect to ETBR-LP2

C. Intracellular IP3 Accumulation Assay

On day 1, cells comprising the serotonin receptors (endogenous and mutated) were plated onto 24 well plates, usually 1×10^5 cells/well. On day 2 cells were transfected by firstly mixing 0.25ug DNA in 50 ul serumfree DMEM/well and 2 ul lipofectamine in 50 ul serumfree DMEM/well. The solutions were gently mixed and incubated for 15-30 min at room temperature. Cells were washed with 0.5 ml PBS and 400 ul of serum free media was mixed with the transfection media and added to the cells. The cells were then incubated for 3-4 hrs at $37^\circ\text{C}/5\%\text{CO}_2$ and then the transfection media was removed and replaced with 1ml/well of regular growth media. On day 3 the cells were labeled with ^3H -myo-inositol. Briefly, the media was removed the cells were washed with 0.5 ml PBS. Then 0.5 ml inositol-free/serumfree media (GIBCO BRL) was added/well with 0.25 μCi of ^3H -myo-inositol / well

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and the cells were incubated for 16-18 hrs o/n at 37°C/5%CO₂. On Day 4 the cells were washed with 0.5 ml PBS and 0.45 ml of assay medium was added containing inositol-free/serum free media 10 µM pargyline 10 mM lithium chloride or 0.4 ml of assay medium and 50 µl of 10x ketanserin (ket) to final concentration of 10µM. The cells were then
5 incubated for 30 min at 37°C. The cells were then washed with 0.5 ml PBS and 200 µl of fresh/icecold stop solution (1M KOH; 18 mM Na-borate; 3.8 mM EDTA) was added/well. The solution was kept on ice for 5-10 min or until cells were lysed and then neutralized by 200 µl of fresh/ice cold neutralization sol. (7.5 % HCL). The lysate was then transferred into 1.5 ml eppendorf tubes and 1 ml of chloroform/methanol (1:2) was added/tube. The solution
10 was vortexed for 15 sec and the upper phase was applied to a Biorad AG1-X8 anion exchange resin (100-200 mesh). Firstly, the resin was washed with water at 1:1.25 W/V and 0.9 ml of upper phase was loaded onto the column. The column was washed with 10 mls of 5 mM myo-inositol and 10 ml of 5 mM Na-borate/60mM Na-formate. The inositol tris phosphates were eluted into scintillation vials containing 10 ml of scintillation cocktail with
15 2 ml of 0.1 M formic acid/ 1 M ammonium formate. The columns were regenerated by washing with 10 ml of 0.1 M formic acid/3M ammonium formate and rinsed twice with dd H₂O and stored at 4°C in water.

Figure 7 provides an illustration of IP3 production from the human 5-HT_{2A} receptor that incorporates the C322K mutation. While these results evidence that the Proline Mutation
20 Algorithm approach constitutively activates this receptor, for purposes of using such a receptor for screening for identification of potential therapeutics, a more robust difference would be preferred. However, because the activated receptor can be utilized for understanding and elucidating the role of constitutive activation and for the identification of compounds that

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can be further examined, we believe that this difference is itself useful in differentiating between the endogenous and non-endogenous versions of the human 5HT_{2A} receptor.

D. Result Summary

The results for the GPCRs tested are set forth in Table E where the Per-Cent Increase indicates the percentage difference in results observed for the non-endogenous GPCR as compared to the endogenous GPCR; these values are followed by parenthetical indications as to the type of assay utilized. Additionally, the assay system utilized is parenthetically listed (and, in cases where different Host Cells were used, both are listed). As these results indicate, a variety of assays can be utilized to determine constitutive activity of the non-endogenous versions of the human GPCRs.

Those skilled in the art, based upon the foregoing and with reference to information available to the art, are credited with the ability to select and/or maximize a particular assay approach that suits the particular needs of the investigator.

Table E

Receptor Identifier (Codon Mutation)	Per-Cent Difference
GPR17 (V234K)	74.5 (CRE-Luc)
GPR30 (L258K)	71.6 (CREB)
APJ (L247K)	49.0 (GTP _γ S)
ETBR-LP2 (N358K)	48.4(AP1-Luc - 293) 61.1(AP1-Luc - 293T)
GHSR (V262K)	58.9(CREB - 293) 35.6(CREB - 293T)

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MIG (I230K)	39 (cAMP)
Serotonin 5HT _{2A} (C322K)	33.2 (IP ₃)
Serotonin 5HT _{2C} (S310K)	39.1 (IP ₃)

5

Example 6**Tissue Distribution of Endogenous Orphan GPCRs**

Using a commercially available human-tissue dot-blot format, endogenous orphan GPCRs were probed for a determination of the areas where such receptors are localized. Except as indicate below, the entire receptor cDNA (radiolabelled) was used as the probe: radiolabeled probe was generated using the complete receptor cDNA (excised from the vector) using a Prime-It II™ Random Primer Labeling Kit (Stratagene, #300385), according to manufacturer's instructions. A human RNA Master Blot™ (Clontech, #7770-1) was hybridized with the GPCR radiolabeled probe and washed under stringent conditions according manufacturer's instructions. The blot was exposed to Kodak BioMax Autoradiography film overnight at - 80°C.

15

Representative dot-blot format results are presented in Figure 8 for GPR1 (8A), GPR30 (8B), and APJ (8C), with results being summarized for all receptors in Table F

20

Table F

GPCR	Tissue Distribution (highest levels, relative to other tissues in the dot-blot)
GPR1	Placenta, Ovary, Adrenal

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5

10

15

20

GPR4	Broad; highest in Heart, Lung, Adrenal, Thyroid, Spinal Cord
GPR5	Placenta, Thymus, Fetal Thymus Lesser levels in spleen, fetal spleen
GPR7	Liver, Spleen, Spinal Cord, Placenta
GPR8	No expression detected
GPR9-6	Thymus, Fetal Thymus Lesser levels in Small Intestine
GPR18	Spleen, Lymph Node, Fetal Spleen, Testis
GPR20	Broad
GPR21	Broad; very low abundance
GPR22	Heart, Fetal Heart Lesser levels in Brain
GPR30	Stomach
GPR31	Broad
BLR1	Spleen
CEPR	Stomach, Liver, Thyroid, Putamen
EBI1	Pancreas Lesser levels in Lymphoid Tissues
EBI2	Lymphoid Tissues, Aorta, Lung, Spinal Cord
ETBR-LP2	Broad; Brain Tissue
GPCR-CNS	Brain Lesser levels in Testis, Placenta
GPR-NGA	Pituitary Lesser levels in Brain
H9	Pituitary
HB954	Aorta, Cerebellum Lesser levels in most other tissues
HM74	Spleen, Leukocytes, Bone marrow, Mammary Glands, Lung, Trachea
MIG	Low levels in Kidney, Liver, Pancreas, Lung, Spleen
ORG1	Pituitary, Stomach, Placenta
V28	Brain, Spleen, Peripheral Leukocytes

25

Based upon the foregoing information, it is noted that human GPCRs can also be assessed for distribution in diseased tissue; comparative assessments between "normal" and diseased tissue can then be utilized to determine the potential for over-expression or under-expression of a particular receptor in a diseased state. In those circumstances where it is desirable to utilize the non-endogenous versions of the human GPCRs for the purpose of screening to directly identify

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candidate compounds of potential therapeutic relevance, it is noted that inverse agonists are useful in the treatment of diseases and disorders where a particular human GPCR is over-expressed, whereas agonists or partial agonists are useful in the treatment of diseases and disorders where a particular human GPCR is under-expressed.

5 As desired, more detailed, cellular localization of the receptors, using techniques well-known to those in the art (e.g., in-situ hybridization) can be utilized to identify particular cells within these tissues where the receptor of interest is expressed.

It is intended that each of the patents, applications, and printed publications mentioned in this patent document be hereby incorporated by reference in their entirety.

10 As those skilled in the art will appreciate, numerous changes and modifications may be made to the preferred embodiments of the invention without departing from the spirit of the invention. It is intended that all such variations fall within the scope of the invention.

Although a variety of expression vectors are available to those in the art, for purposes of utilization for both the endogenous and non-endogenous human GPCRs, it is most preferred that
15 the vector utilized be pCMV. This vector has been deposited with the American Type Culture Collection (ATCC) on October 13, 1998 (10801 University Blvd., Manassas, VA 20110-2209 USA) under the provisions of the Budapest Treaty for the International Recognition of the Deposit of Microorganisms for the Purpose of patent Procedure. The vector was tested by the ATCC on _____, 1998 and determined to be viable on _____, 1998. The ATCC has assigned
20 the following deposit number to pCMV: _____.

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CLAIMS

What is claimed is:

1. A constitutively active, non-endogenous version of an endogenous human orphan G protein-coupled receptor (GPCR) comprising the following amino acid residues (carboxy-terminus to amino-terminus orientation) transversing the transmembrane-6 (TM6) and intracellular loop-3 (IC3) regions of the non-endogenous GPCR:

P¹ AA₁₅ X

wherein:

- 10 (1) P¹ is an amino acid residue located within the TM6 region of the non-endogenous GPCR, where P¹ is selected from the group consisting of (i) the endogenous orphan GPCR proline residue, and (ii) a non-endogenous amino acid residue other than proline;
- 15 (2) AA₁₅ are 15 amino acid residues selected from the group consisting of (a) the 15 endogenous amino acid residues of the endogenous orphan GPCR, (b) 15 non-endogenous amino acid residues, and (c) a combination of 15 amino acid residues, the combination comprising at least one endogenous amino acid residue of the endogenous orphan GPCR and at least one non-endogenous amino acid residue, excepting that none of the 15 endogenous amino acid residues that are positioned within the TM6 region of the GPCR is proline; and
- 20 (2) X is a non-endogenous amino acid residue located within the IC3 region of said non-endogenous GPCR.

2. The non-endogenous human GPCR of claim 1 wherein P¹ is the endogenous proline

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residue.

3. The non-endogenous human GPCR of claim 1 wherein P¹ is a non-endogenous amino acid residue other than a proline residue.
4. The non-endogenous human GPCR of claim 1 wherein AA₁₅ are the 15 endogenous amino acid residues of the endogenous GPCR.
5. The non-endogenous human GPCR of claim 1 wherein X is selected from the group consisting of lysine, histidine, arginine and alanine residues, excepting that when the endogenous amino acid in position X of said endogenous human GPCR is lysine, X is selected from the group consisting of histidine, arginine and alanine.
- 10 6. The non-endogenous human GPCR of claim 1 wherein X is a lysine residue, excepting that when the endogenous amino acid in position X of said endogenous human GPCR is lysine, X is an amino acid other than lysine.
7. The non-endogenous human GPCR of claim 4 wherein X is a lysine residue, excepting that when the endogenous amino acid in position X of said endogenous human GPCR is lysine, X is an amino acid other than lysine.
- 15 8. The non-endogenous, human GPCR of claim 1 wherein P¹ is a proline residue and X is a lysine residue, excepting that when the endogenous amino acid in position X of said endogenous human GPCR is lysine, X is an amino acid other than lysine.
9. A host cell comprising the non-endogenous human GPCR of claim 1.
- 20 10. The material of claim 9 wherein said host cell is of mammalian origin.
11. The non-endogenous human GPCR of claim 1 in a purified and isolated form.
12. A nucleic acid sequence encoding a constitutively active, non-endogenous version of an endogenous human orphan G protein-coupled receptor (GPCR) comprising the following

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nucleic acid sequence region transversing the transmembrane-6 (TM6) and intracellular loop-3 (IC3) regions of the orphan GPCR:



wherein:

- 5 (1) P_{codon} is a nucleic acid encoding region within the TM6 region of the non-endogenous GPCR, where P_{codon} encodes an amino acid selected from the group consisting of (i) the endogenous GPCR proline residue, and (ii) a non-endogenous amino acid residue other than proline;
 - 10 (2) $(\text{AA-codon})_{15}$ are 15 codons encoding 15 amino acid residues selected from the group consisting of (a) the 15 endogenous amino acid residues of the endogenous orphan GPCR, (b) 15 non-endogenous amino acid residues, and (c) a combination of 15 amino acid residues, the combination comprising at least one endogenous amino acid residue of the endogenous orphan GPCR and at least one non-
15 endogenous amino acid residue, excepting that none of the 15 endogenous amino acid residues that are positioned within the TM6 region of the orphan GPCR is proline; and
 - 20 (3) X_{codon} is a nucleic acid encoding region residue located within the IC3 region of said non-endogenous human GPCR, where X_{codon} encodes a non-endogenous amino acid.
13. The nucleic acid sequence of claim 12 wherein P_{codon} encodes an endogenous proline residue.
 14. The nucleic acid sequence of claim 12 wherein P_{codon} encodes a non-endogenous

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amino acid residue other than a proline residue.

15. The nucleic acid sequence of claim 12 wherein X_{codon} encodes a non-endogenous amino acid selected from the group consisting of lysine, histidine, arginine and alanine, excepting that when the endogenous amino acid in position X of said endogenous human GPCR is lysine, X_{codon} encodes an amino acid selected from the group consisting of histidine, arginine and alanine.
16. The nucleic acid sequence of claim 13 wherein X_{codon} encodes a non-endogenous lysine amino acid excepting that when the endogenous amino acid in position X of said endogenous human GPCR is lysine, X_{codon} encodes an amino acid selected from the group consisting of histidine, arginine and alanine.
17. The nucleic acid sequence of claim 12 wherein X_{codon} is selected from the group consisting of AAA, AAG, GCA, GCG, GCC and GCU.
18. The nucleic acid sequence of claim 12 wherein X_{codon} is selected from the group consisting of AAA and AAG.
19. The nucleic acid sequence of claim 12 wherein P_{codon} is selected from the group consisting of CCA, CCC, CCG and CCU, and X_{codon} is selected from the group consisting of AAA and AAG.
20. A vector comprising the nucleic acid sequence of claim 12.
21. A plasmid comprising the nucleic acid sequence of claim 12.
22. A host cell comprising the nucleic acid sequence of claim 21.
23. The nucleic acid sequence of claim 12 in a purified and isolated form.
24. A method for selecting for alteration an endogenous amino acid residue within the third intracellular loop of a human G protein-coupled receptor ("GPCR"), said receptor

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comprising a transmembrane 6 region and an intracellular loop 3 region, which endogenous amino acid, when altered to a non-endogenous amino acid, constitutively activates said human GPCR, comprising the following steps:

- 5 (a) identifying an endogenous proline residue within the transmembrane 6 region of a human GPCR;
 - (b) identifying, by moving in a direction of the carboxy-terminus region of said GPCR towards the amino-terminus region of said GPCR, the endogenous, 16th amino acid residue from said proline residue;
 - (c) altering the endogenous residue of step (b) to a non-endogenous amino acid
10 residue to create a non-endogenous version of an endogenous human GPCR;
and
 - (d) determining whether the non-endogenous human GPCR of step (c) is constitutively active.
25. The method of claim 24 wherein the amino acid residue that is two residues from said
15 proline residue in the transmembrane 6 region, in a carboxy-terminus to amino-terminus direction, is tryptophan.
26. A constitutively active, non-endogenous human GPCR produced by the process of claim 24.
27. A constitutively active, non-endogenous human GPCR produced by the process of
20 claim 25.
28. An algorithmic approach for creating a non-endogenous, constitutively active version of an endogenous human G protein coupled receptor (GPCR), said endogenous GPCR comprising a transmembrane 6 region and an intracellular loop 3 region, the

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algorithmic approach comprising the steps of:

- (a) selecting an endogenous human GPCR comprising a proline residue in the transmembrane-6 region;
 - (b) identifying, by counting 16 amino acid residues from the proline residue of step (a), in a carboxy-terminus to amino-terminus direction, an endogenous amino acid residue;
 - (c) altering the identified amino acid residue of step (b) to a non-endogenous amino acid residue to create a non-endogenous version of the endogenous human GPCR; and
 - (d) determining if the non-endogenous version of the endogenous human GPCR of step (c) is constitutively active.
29. The algorithmic approach of claim 28 wherein the amino acid residue that is two residues from said proline residue in the transmembrane 6 region, in a carboxy-terminus to amino-terminus direction, is tryptophan.
30. A constitutively active, non-endogenous human GPCR produced by the algorithmic approach of claim 28.
31. A constitutively active, non-endogenous human GPCR produced by the algorithmic approach of claim 29.
32. A method for directly identifying a compound selected from the group consisting of inverse agonists, agonists and partial agonists to a non-endogenous, constitutively activated human G protein coupled receptor, said receptor comprising a transmembrane-6 region and an intracellular loop-3 region, comprising the steps of:
- (a) selecting an endogenous human GPCR;

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- (b) identifying a proline residue within the transmembrane-6 region of the GPCR of step (a);
 - (c) identifying, in a carboxy-terminus to amino-terminus direction, the endogenous, 16th amino acid residue from the proline residue of step (b);
 - 5 (d) altering the endogenous amino acid of step (c) to a non-endogenous amino acid;
 - (e) confirming that the non-endogenous GPCR of step (d) is constitutively active;
 - (f) contacting a candidate compound with the non-endogenous, constitutively-activated GPCR of step (e); and
 - 10 (g) determining, by measurement of the compound efficacy at said contacted receptor, whether said compound is an inverse agonist, agonist or partial agonist of said receptor.
-
- 33. The method of claim 32 wherein the non-endogenous amino acid of step (d) is lysine.
 - 34. A compound directly identified by the method of claim 32.
 - 15 35. The method of claim 32 wherein the directly identified compound is an inverse agonist.
 - 36. The method of claim 32 wherein the directly identified compound is an agonist.--
 - 37. The method of claim 32 wherein the directly identified compound is a partial agonist.
 - 38. A composition comprising the inverse agonist of claim 35.
 - 20 39. A composition comprising the agonist of claim 36.
 - 40. A composition comprising the partial agonist of claim 37.
 - 41. A method for directly identifying an inverse agonist to a non-endogenous,

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constitutively activated human G protein coupled receptor ("GPCR"), said GPCR comprising a transmembrane-6 region and an intracellular loop-3 region, comprising the steps of:

- (a) selecting an endogenous human GPCR;
 - (b) identifying a proline residue within the transmembrane-6 region of the GPCR of
5 step (a);
 - (c) identifying, in a carboxy-terminus to amino-terminus direction, the
endogenous, 16th amino acid residue from the proline residue of step (b);
 - (d) altering the endogenous amino acid of step (c) to a non-endogenous lysine residue;
 - (e) confirming that the non-endogenous GPCR of step (d) is constitutively active;
 - 10 (f) contacting a candidate compound with the non-endogenous, constitutively-
activated GPCR of step (e); and
 - (g) determining, by measurement of the compound efficacy at said contacted receptor,
whether said compound is an inverse agonist of said receptor.
42. An inverse agonist directly identified by the method of claim 37.
- 15 43. A composition comprising an inverse agonist of claim 38.

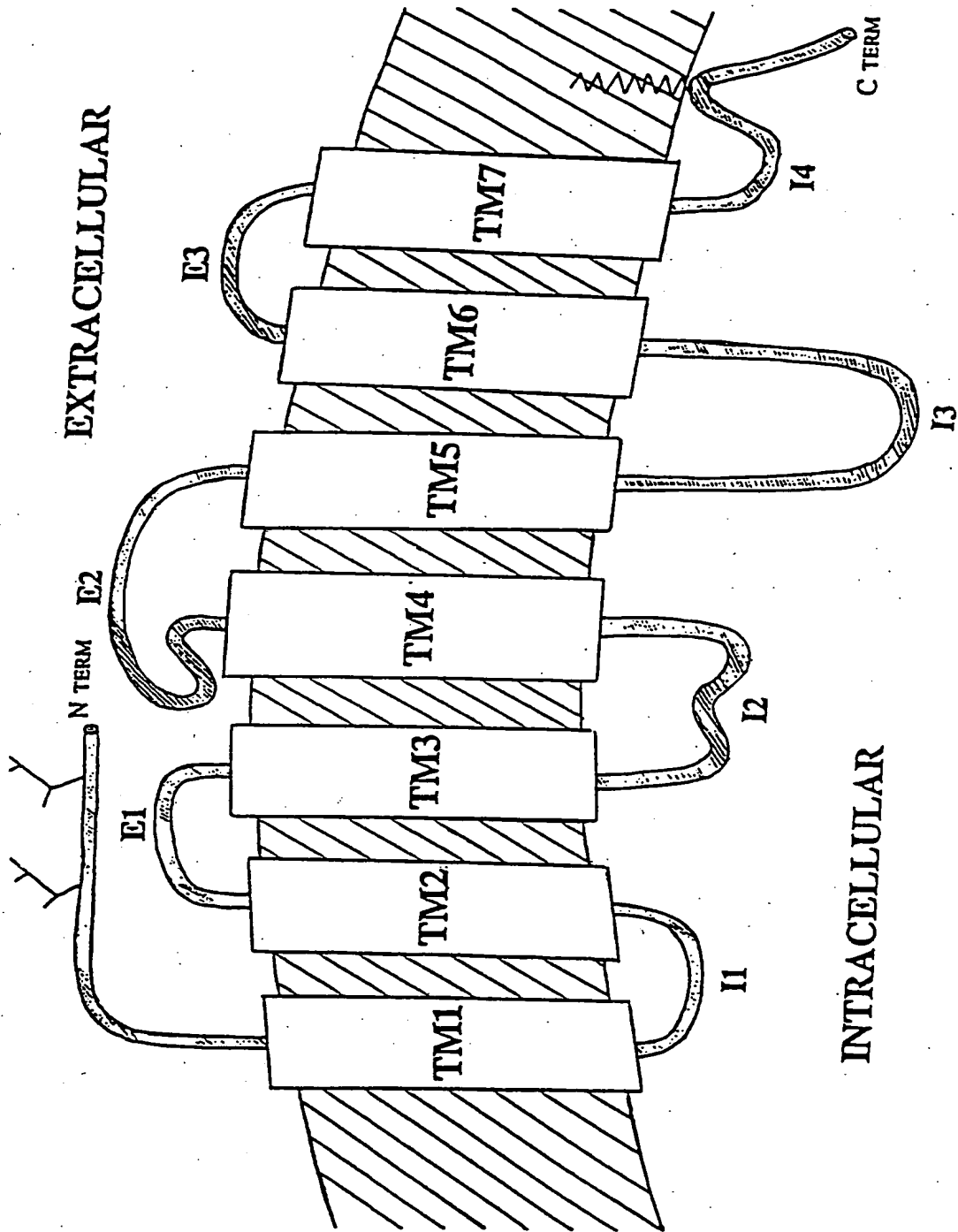


FIGURE 1

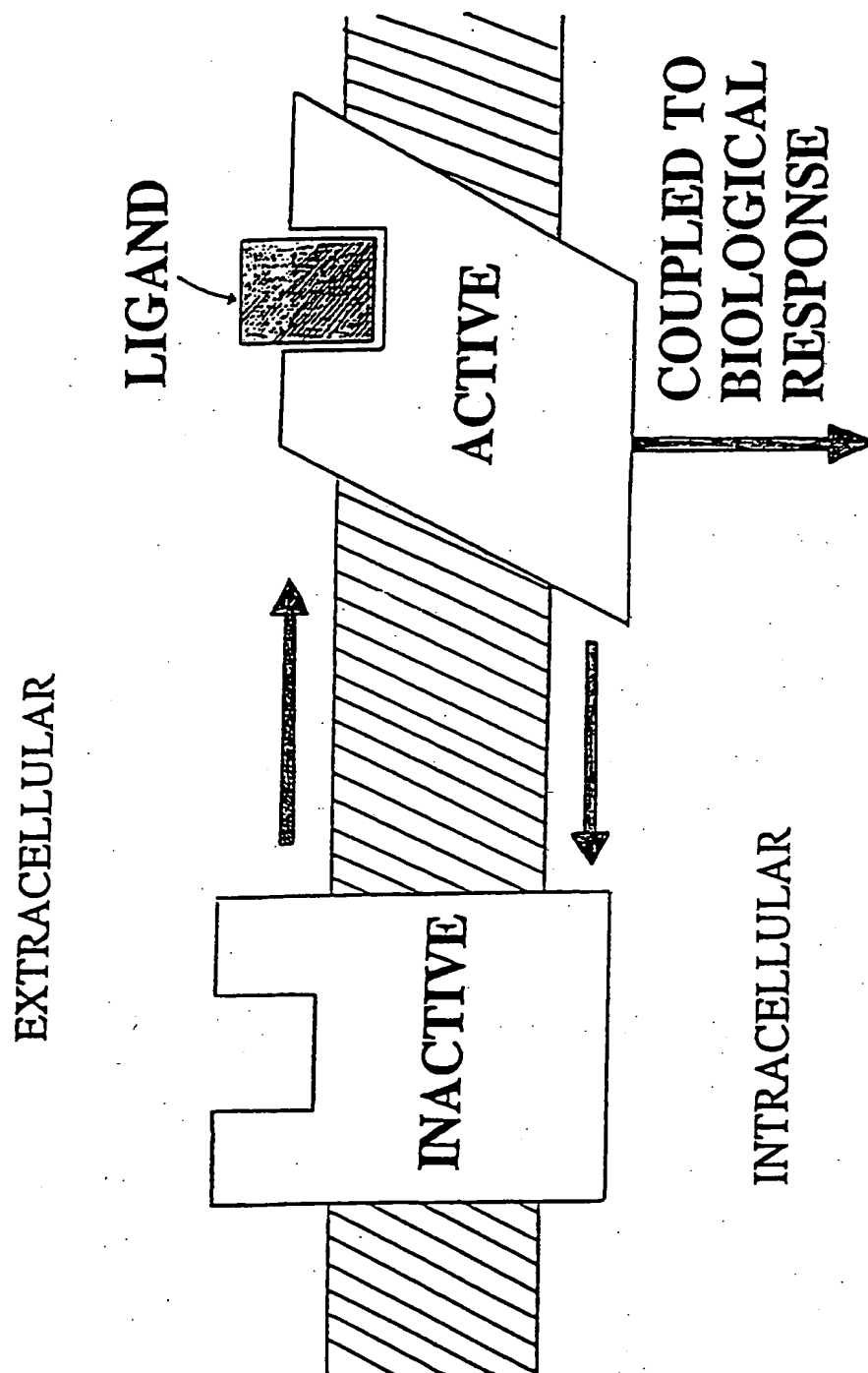


FIGURE 2

pCMV Sequence and Restriction Site

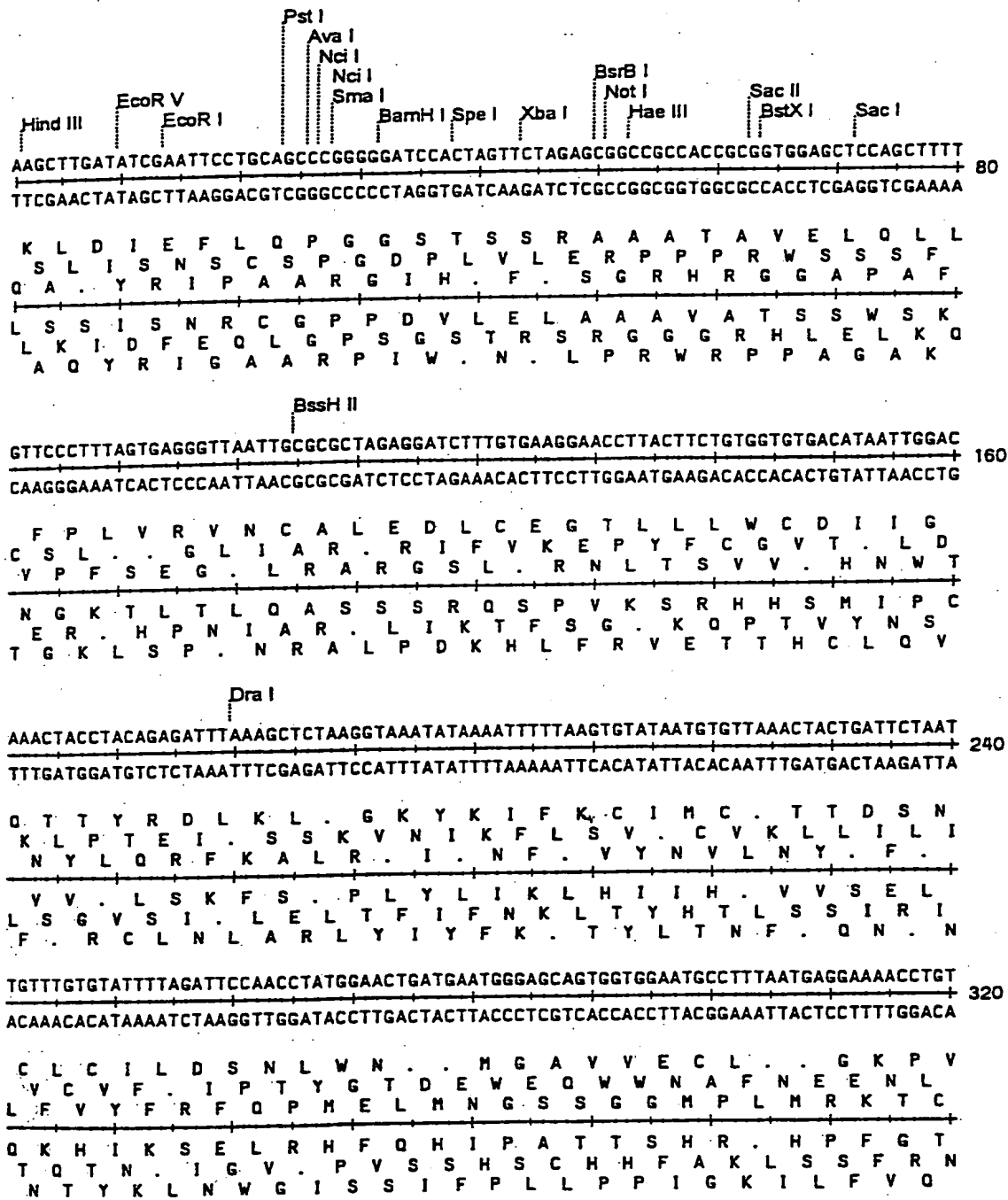


FIGURE 3A

TTTGCTCAGAAGAAATGCCATCTAGTGATGATGAGGCTACTGCTGACTCTCAACATTCTACTCCTCCAAAAAGAAGAGA 400
AAACGAGTCTTCTTTACGGTAGATCACTACTACTCCGATGACGACTGAGAGTTGTAAGATGAGGAGGTTTTTCTCTCT

L L R R N A I G Y C . L S T F Y S S K K E E
F C S E E H P S S D D E A T A D S O H S T P P K K K R
F A Q K K C H L V M M R L L L T L N I L L L Q K R R E
K S L L F A M . H H H P . Q Q S E V N . E E L F S S F
Q E S S I G D L S S S A V A S E . C E V G G F F F L
K A . F F H W R T I I L S S S V R L M R S R W F L L S

Sty I

AAGGTAGAAGACCCCAAGGACTTTCCTTCAGAATTGCTAAGTTTTTGGTTCATGCTGTGTTTAGTAATAGAACTCTTGC 480
TTCCATCTTCTGGGGTTCTGAAAGGAAGTCTTAACGATTCAAAAACTCAGTACGACACAAATCATTATCTTGAGAAGC

K G R R P Q G L S F R I A K F F E S C C V . . . N S C
K V E D P K D F P S E L L S F L S H A V F S N R T L A
R . K T P R T F L Q N C . V F . V M L C L V I E L L
P L L G W P S E K L I A L N K S D H Q T . Y Y F E Q
F T S S G L S K G E S N S L K K L . A T N L L L V R A
L Y F V G L V K R . F Q . T K Q T M S H K T I S S K S

TTGCTTTGCTATTTACACCACAAAGGAAAAAGCTGCACTGCTATACAAGAAAATTATGGAAAAATATTCTGTAACCTTTA 560
AACGAAACGATAAATGTGGTGTTCCTTTTTCGACGTGACGATATGTTCTTTAATACCTTTTTATAAGACATTGGAAT

L L C Y L H K G K S C T A I Q E N Y G K I F C N L Y
C F A I Y T T K E K A A L L Y K K I M E K Y S V T F
L A L L F T P Q R K K L H C Y T R K L W K N I L . P L
K S Q . K C W L P F L Q V A I C S F . P F I N Q L R .
Q K A I . V V F S F A A S S Y L F I I S F Y E T V K I
A K S N V G C L F F S C Q . V L F N H F F I R Y G K

Ase I

TAAGTAGGCATAACAGTTATAATCATAACATACTGTTTTTCTTACTCCACACAGGCATAGAGTGTCTGCTATTAATAAC 640
ATTGATCCGTATTGTCAATATTAGTATTGTATGACAAAAAGAATGAGGTGTGTCGGTATCTCACAGACGATAATTATTG

K . A . Q L . S . H T V F S Y S T Q A . S V C Y .
I S R H N S Y N H N I L F F L T P H R H R V S A I N N
V G I T V I I I T Y C F F L L H T G I E C L L L I T
L Y A Y C N Y D Y C V T K E . E V C A Y L T Q . . Y S
L L C L L . L . L M S N K R V G C L C L T D A I L L
Y T P H V T I I M V Y Q K K K S W V P M S H R S N I V

Rsa I

TATGCTCAAAAATTGTGTACCTTTAGCTTTTTAATTGTAAAGGGTTAATAAGGAATATTTGATGTATAGTGCCTTGAC 720
ATACGAGTTTTTAACACATGGAAATCGAAAAATTAACATTTCCTTATAAACTACATATCACGGAAGT

L C S K I V Y L . L F N L . R G . . G I F D V . C L D
Y A Q K L C T F S F L I C K G V N K E Y L H Y S A L T
H L K N C V P L A F . F V K G L I R N I . C I V P .
H E F I T Y R . S K L K Y L P . Y P I N S T Y H R S
A . F N H V K L K K I Q L P T L L S Y K I Y L A K V
I S L F Q T G K A K . N T F P N I L F I O H I T G Q S

FIGURE 3B

FIGURE 3C

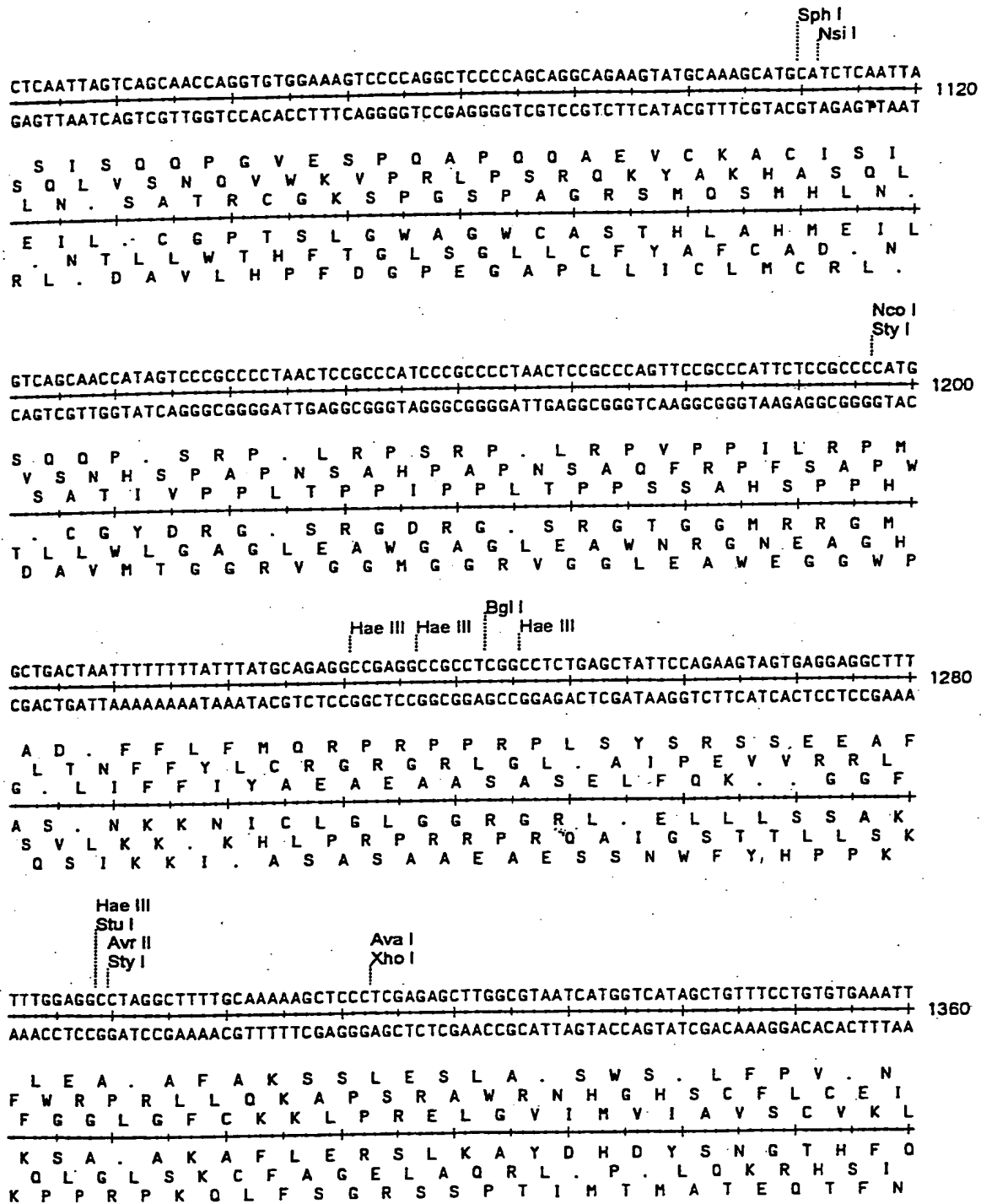


FIGURE 3D

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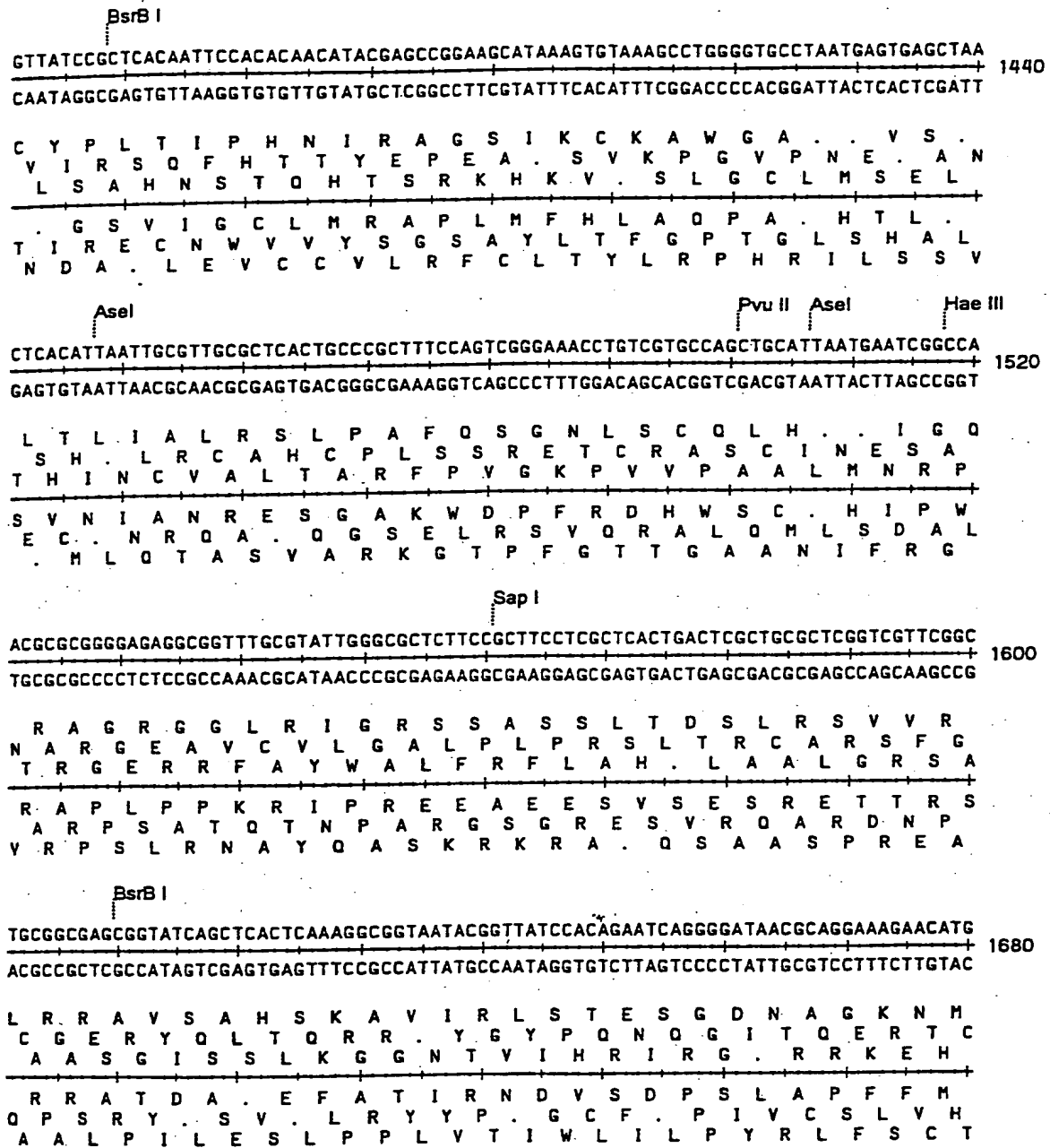


FIGURE 3F

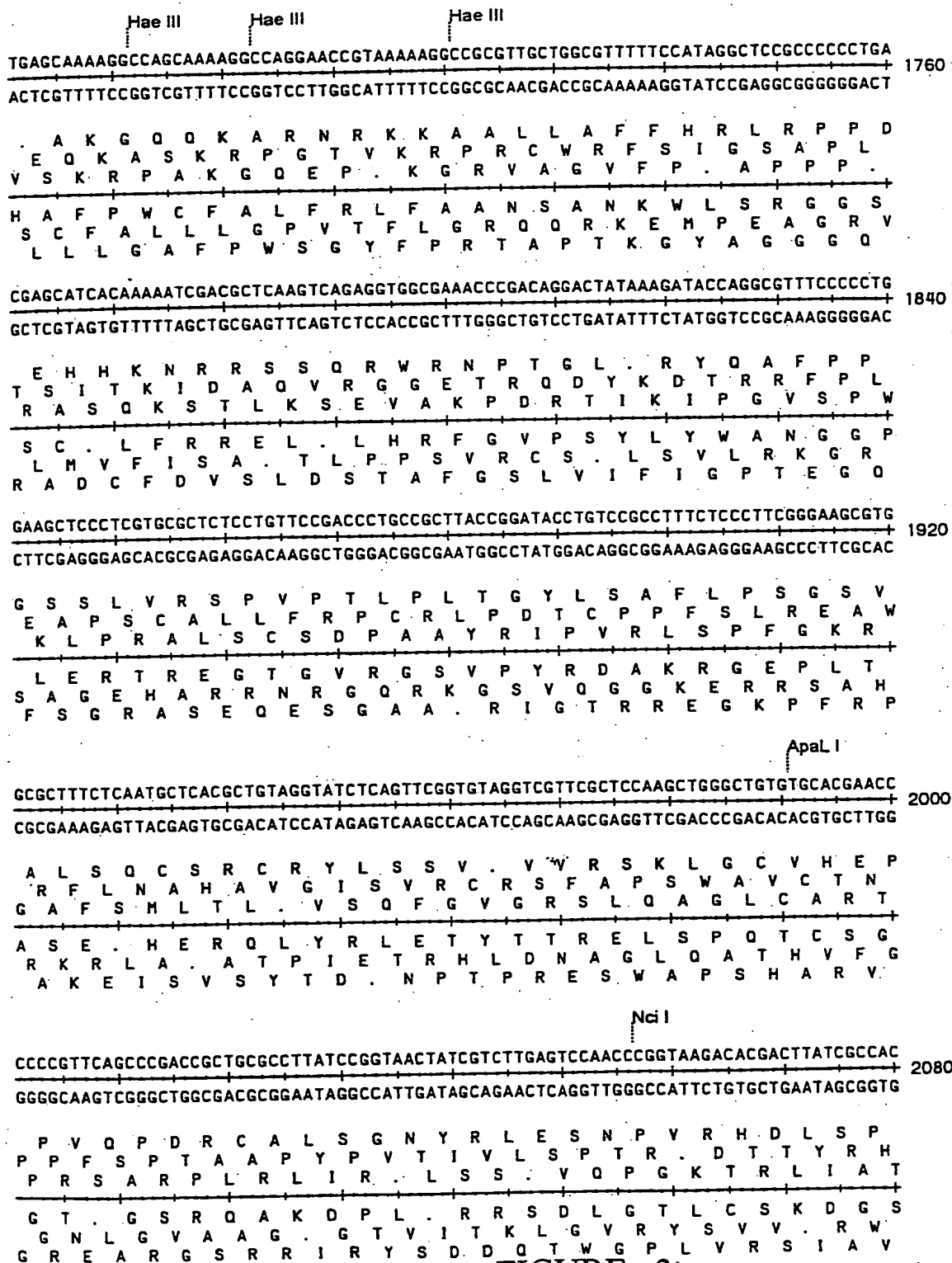


FIGURE 3F

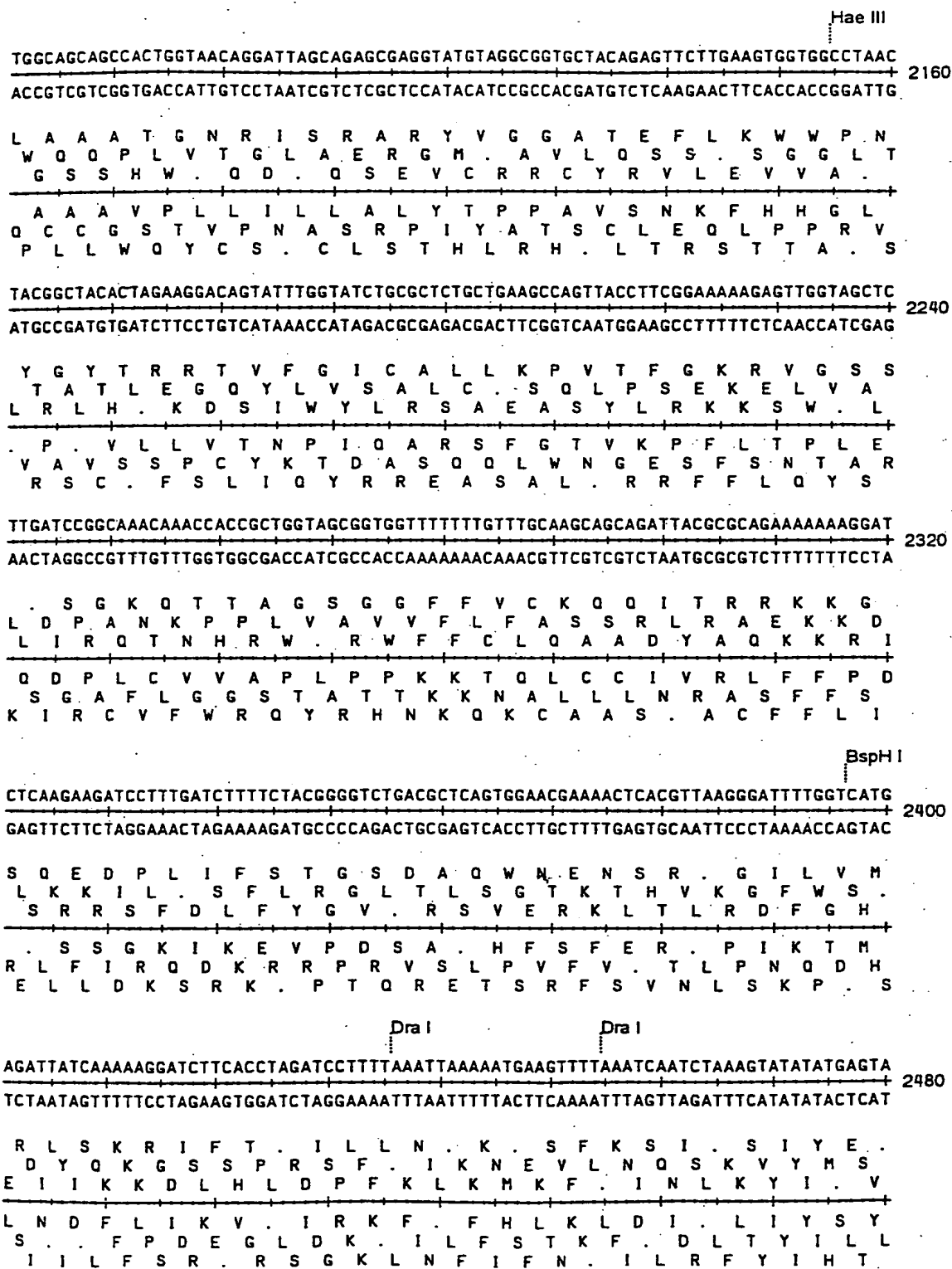


FIGURE 36

AACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTTCGTTTCATCCATAGTTG
TTGAACCAGACTGTCAATGGTTACGAATTAGTCACTCCGTTGGATAGAGTCGCTAGACAGATAAAGCAAGTAGGTATCAAC 2560

T W S D S Y O C L I S E A P I S A I C L F R S S I V
K L G L T V T N A . S V R H L S O R S V Y F V H P . L
N L V . O L P M L N O . G T Y L S D L S I S F I H S C
V O D S L . W H K I L S A G I E A I O R N R E D M T A
S P R V T V L A . D T L C R D . R D T . K T . G Y N
F K T O C N G I S L . H P V . R L S R D I E N M W L O

Hae III
CCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGAC
GGACTGAGGGGCGAGCACATCTATTGATGCTATGCCCTCCGAATGGTAGACCGGGTCAGGACGTTACTATGGCGCTCTG 2640

A . L P V V . I T T I R E G L P S G P S A A M I P R D
P D S P S C R . L R Y G R A Y H L A P V L O . Y R E T
L T P R R V D N Y D T G G L T I W P O C C N D T A R
Q S G T T Y I V V I R S P K G D P G L A A I I G R S
G S E G D H L Y S R Y P L A . W R A G T S C H Y R S V
R V G R R T S L . S V P P S V M O G W H O L S V A L G

Bgl I Hae III Ava II
CCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCTCTGCAACTTT
GGTGGAGTGGCCGAGGTCTAAATAGTCGTTATTGGTCGGTCGGCCTTCCCGCTCGCGTCTTACCAGGACGTTGAAA 2720

P R S P A P D L S A I N O P A G R A E R R S G P A T L
H A H R L O I Y O O . T S O P E G P S A E V V L O L
P T L T G S R F I S N K P A S R K G R A O K W S C N F
G R E G A G S K D A I F W G A P L A S R L L P G A V K
W A . R S W I . C Y V L W G S P G L A S T T R C S .
V S V P E L N I L L L G A L R F P R A C F H D O L K

Asel Nci I Fsp I
ATCCGCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTG
TAGGCGGAGGTAGGTGAGATAATTAACAACGGCCCTTCGATCTCATTCAATCAAGCGGTCAATTATCAAACGCGTTGCAAC 2800

S A S I O S I N C C R E A R V S S S P V N S L R N V
Y P P P S S L I V A G K L E . V V R O L I V C A T L
I R L H P V Y . L L P G S . S K . F A S . . F A O R C
D A E H W D I L O O R S A L T L L E G T L L K R L T T
G G G D L R N I T A P F S S Y T T R W N I T O A V N
I R R W G T . . N N G P L . L L Y N A L . Y N A C R O

TGCCATTGCTACAGGCATCGTGGTGTACGCTCGTCGTTTGGTATGGCTTCATTGAGTCCGGTTCCTCAACGATCAAGG
ACGGTAACGATGTCGTTAGCACCACAGTGCGAGCAGCAAAACCATACCGAAGTAAGTCGAGGCCAAGGGTTGCTAGTTCC 2880

A I A T G I V V S R S S F G M A S F S S G S O R S R
L P L L O A S W C H A R R L V W L H S A P V P N D O G
C H C Y R H R G V T L V V W Y G F I O L R F P T I K
A H A V P M T T D R E D N P I A E N L E P E W R D L
G N S C A D H H . A R R K T H S . E A G T G L S . P
O W O . L C R P T V S T T O

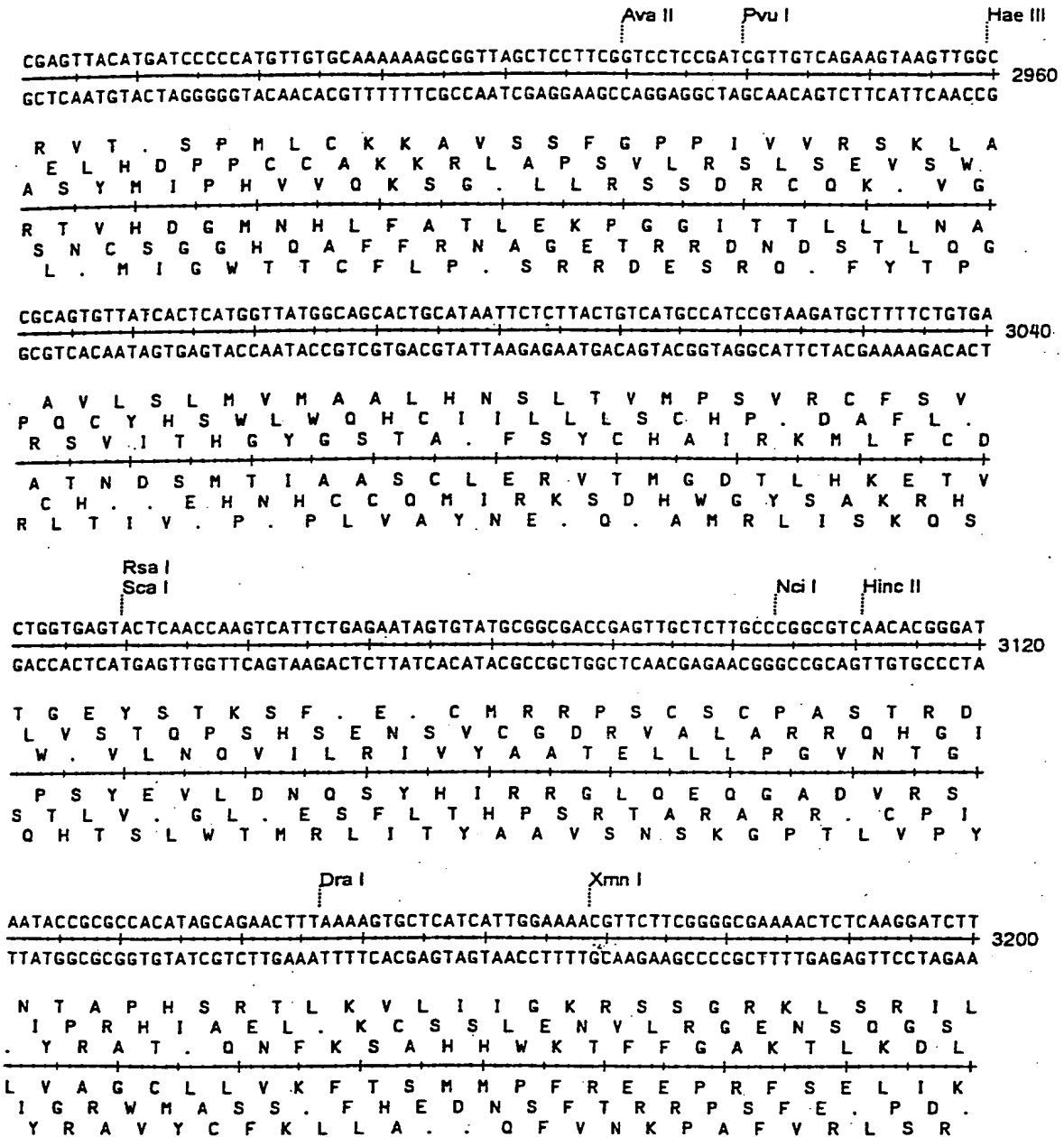


FIGURE 3I

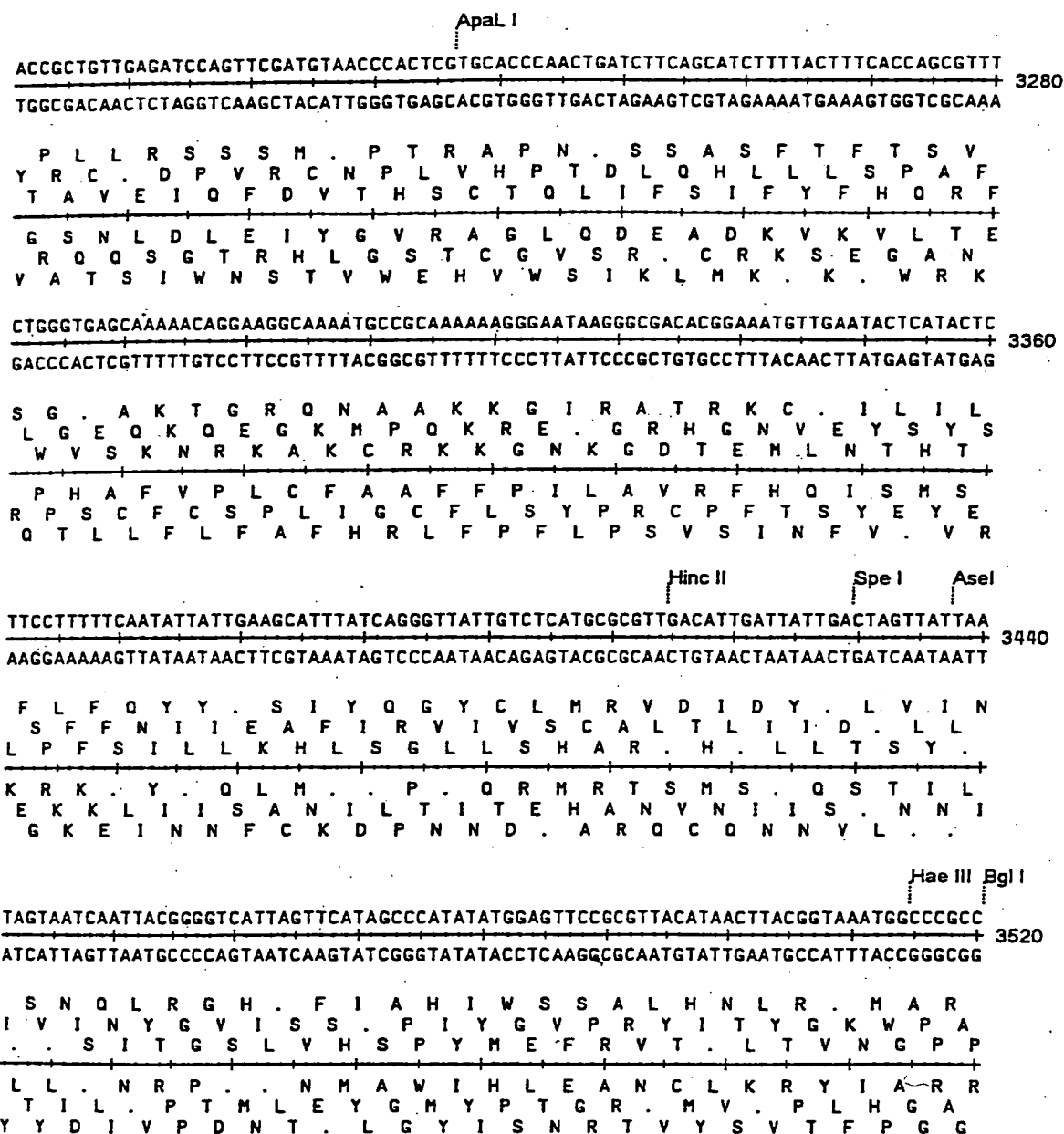


FIGURE 3J

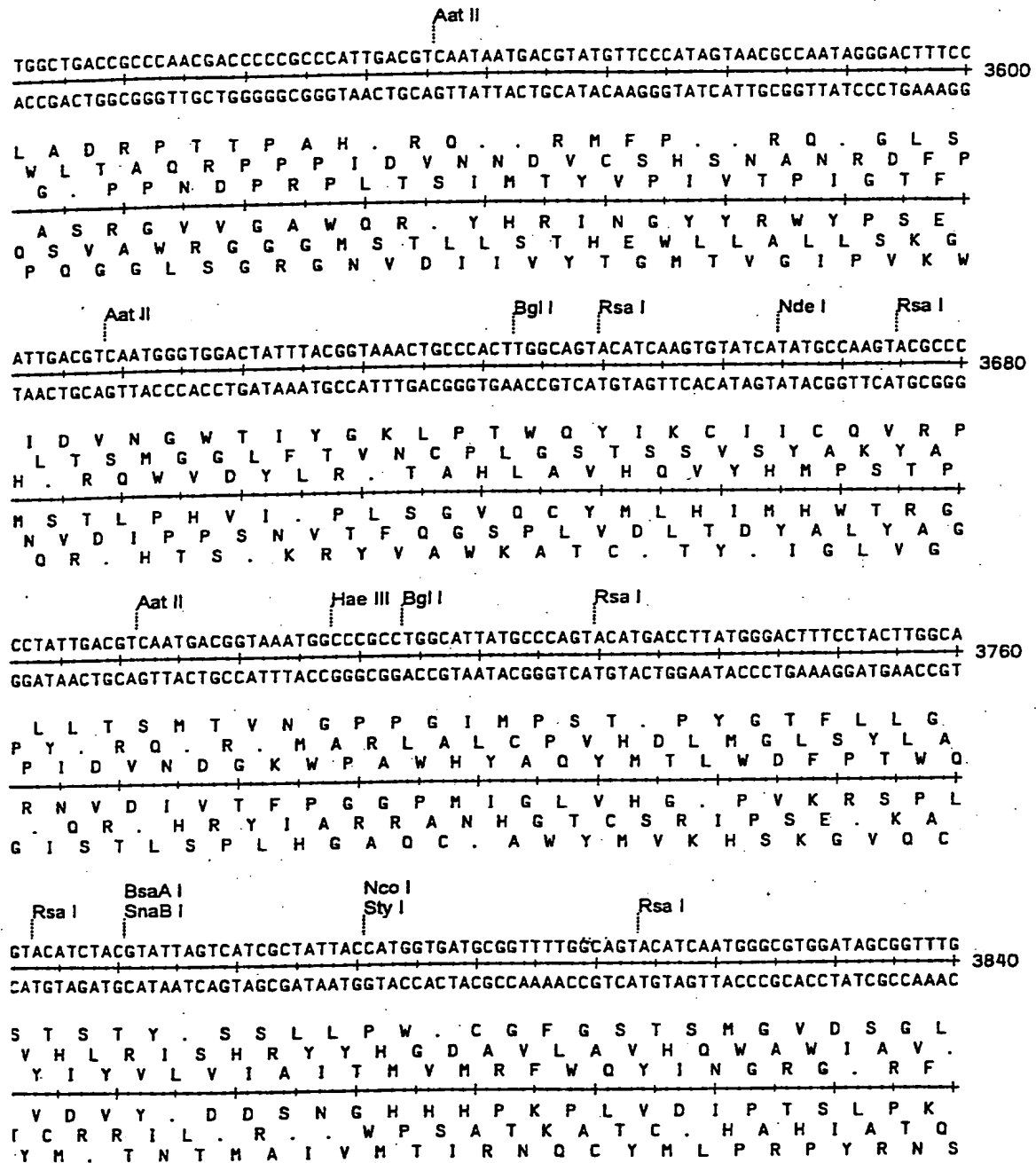


FIGURE 3K

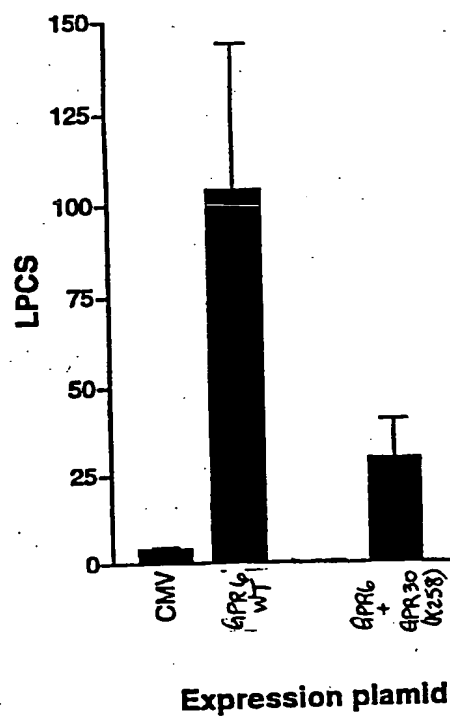


FIGURE 4

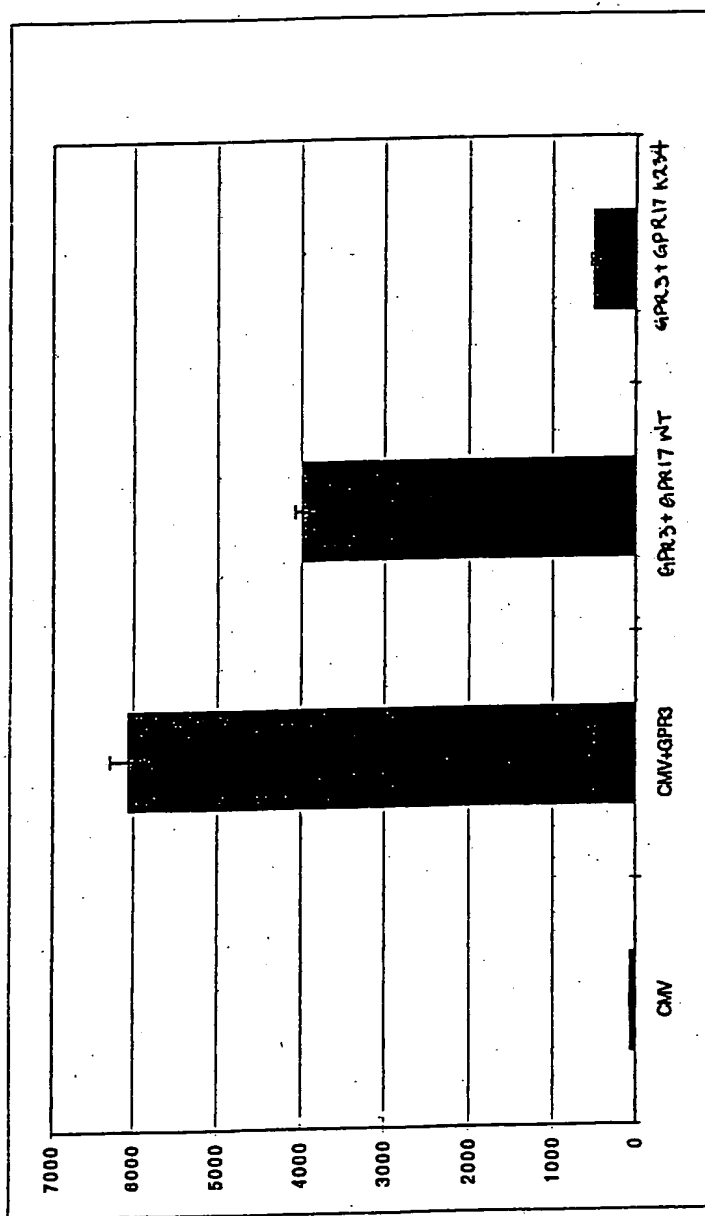


FIGURE 5

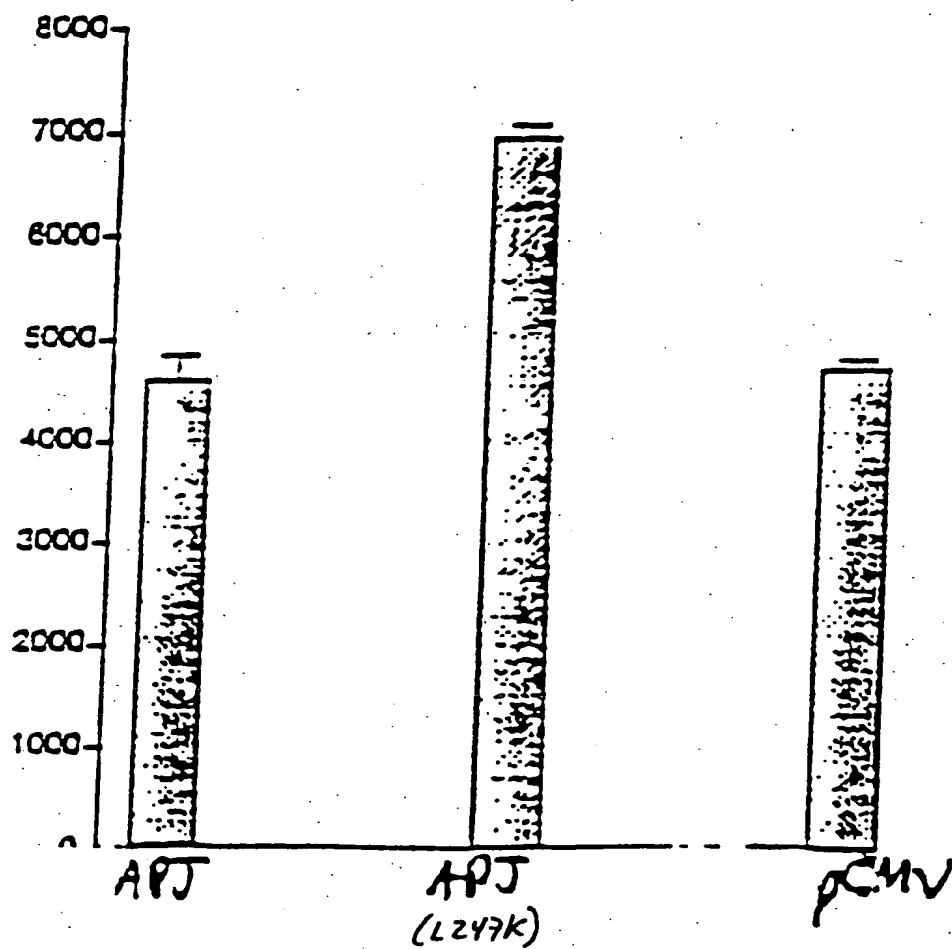


FIGURE 6

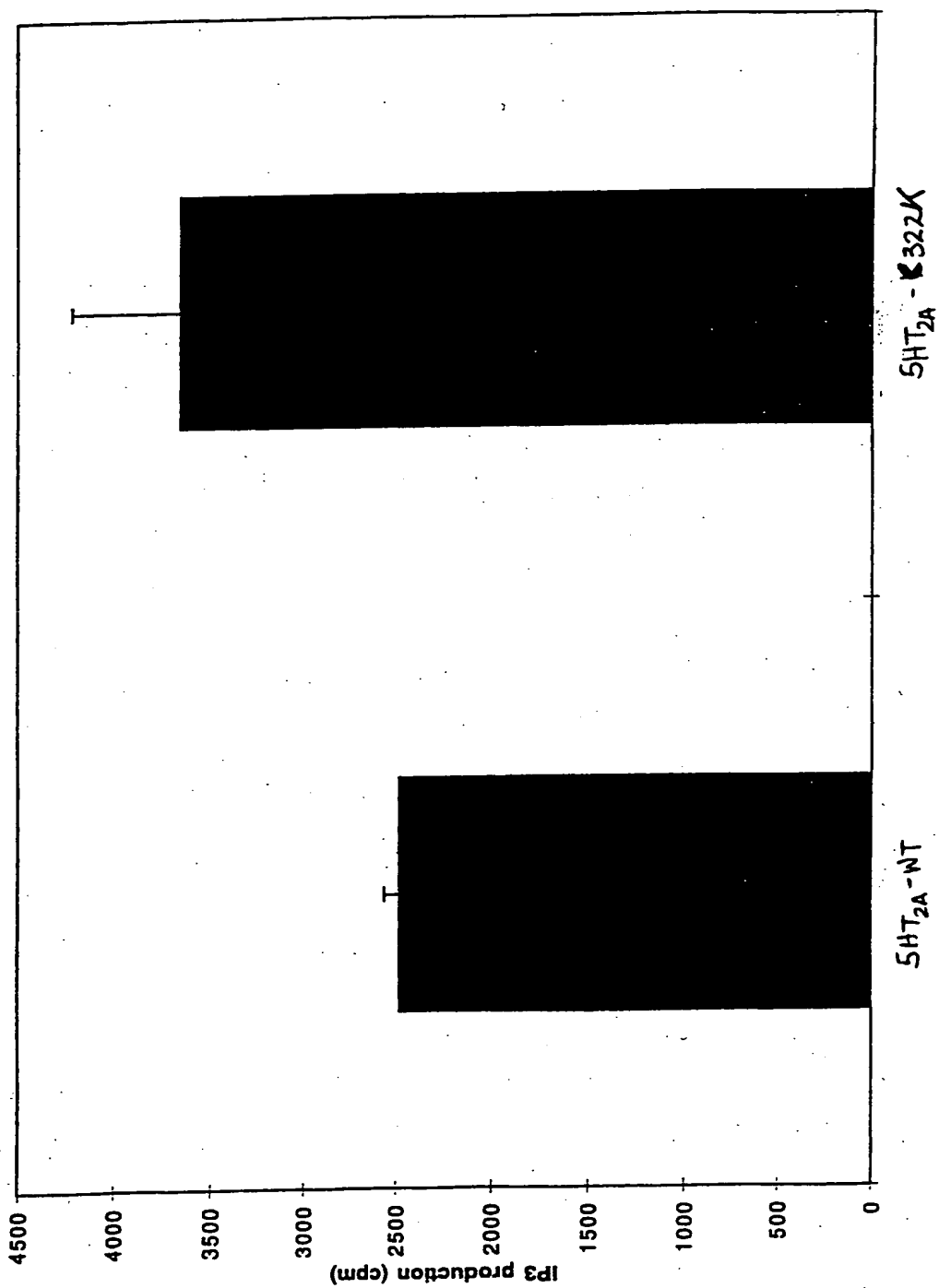


FIGURE 7

FIGURE 8A

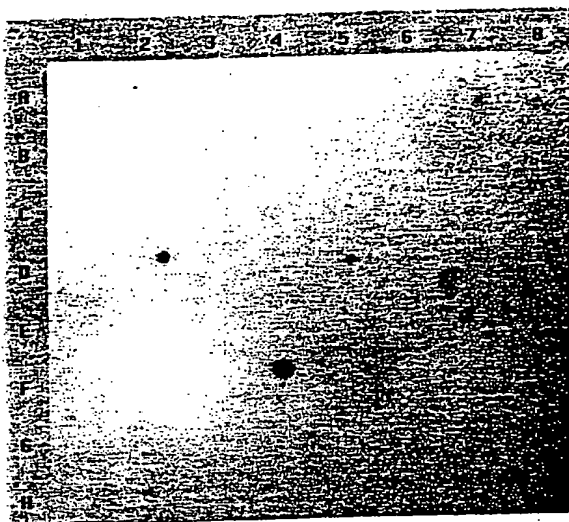


FIGURE 8B

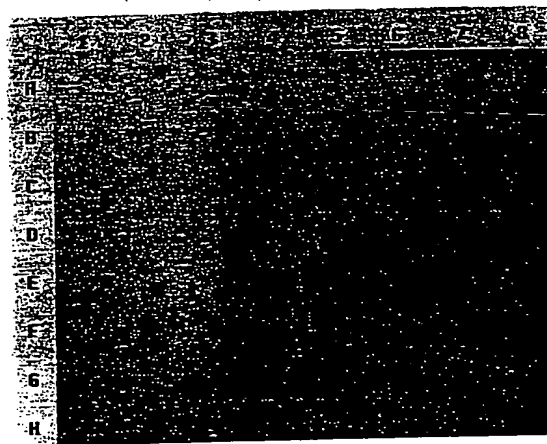
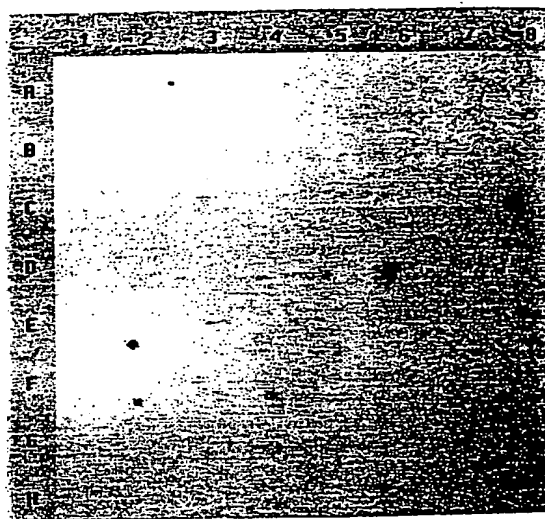


FIGURE 8C

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Behan, Dominic P.
Chalmers, Derek T.
Liaw, Chen W.
- (ii) TITLE OF INVENTION: Non-Endogenous, Constitutively
Activated Human G Protein-Coupled
Orphan Receptors
- 10 (iii) NUMBER OF SEQUENCES: 280
- (iv) CORRESPONDENCE ADDRESS:
- 15 (A) ADDRESSEE: Arena Pharmaceuticals, Inc.
(B) STREET: 6166 Nancy Ridge Drive
(C) CITY: San Diego
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 92122
- 20 (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
- 25 (A) APPLICATION NUMBER: US
(B) FILING DATE:
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Burgoon, Richard P.
(B) REGISTRATION NUMBER: 34,787
- 30 (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: (619) 453-7200
(B) TELEFAX: (619) 453-7210

(2) INFORMATION FOR SEQ ID NO:1:

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1068 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGGAAGATT TGGAGGAAAC ATTATTGAA GAATTTGAAA ACTATTCCTA TGACCTAGAC

TATTACTCTC TGGAGTCTGA TTTGGAGGAG AAAGTCCAGC TGGGAGTTGT TCACTGGGTC 120
 TCCCTGGTGT TATATTGTTT GGCTTTTGTT CTGGGAATTC CAGGAAATGC CATCGTCATT 180
 TGGTTCACGG GGCTCAAGTG GAAGAAGACA GTCACCACTC TGTGGTTCCT CAATCTAGCC 240
 ATTGCGGATT TCATTTTCT TCTCTTCTG CCCCTGTACA TCTCCTATGT GGCCATGAAT 300
 5 TTCCACTGGC CCTTTGGCAT CTGGCTGTGC AAAGCCAATT CCTTCACTGC CCAGTTGAAC 360
 ATGTTTGCCA GTGTTTTTTT CCTGACAGTG ATCAGCCTGG ACCACTATAT CCACTTGATC 420
 CATCCTGTCT TATCTCATCG GCATCGAACC CTCAAGAACT CTCTGATTGT CATTATATTC 480
 ATCTGGCTTT TGGCTTCTCT AATTGGCGGT CCTGCCCTGT ACTTCCGGGA CACTGTGGAG 540
 TTCAATAATC ATACTCTTG CTATAACAAT TTTCAGAAGC ATGATCCTGA CCTCACTTTG 600
 10 ATCAGGCACC ATGTTCTGAC TTGGGTGAAA TTTATCATTG GCTATCTCTT CCCTTTGCTA 660
 ACAATGAGTA TTTGCTACTT GTGTCTCATC TTCAAGGTGA AGAAGCGAAC AGTCCTGATC 720
 TCCAGTAGGC ATTTCTGGAC AATTCTGGTT GTGGTTGTGG CCTTTGTGGT TTGCTGGACT 780
 CCTTATCACC TGTTTAGCAT TTGGGAGCTC ACCATTCAAC ACAATAGCTA TTCCCACCAT 840
 GTGATGCAGG CTGGAATCCC CCTCTCCACT GGTTTGGCAT TCCTCAATAG TTGCTTGAAC 900
 15 CCCATCCTTT ATGTCCTAAT TAGTAAGAAG TTCCAAGCTC GCTTCCGGTC CTCAGTTGCT 960
 GAGATACTCA AGTACACACT GTGGGAAGTC AGCTGTTCTG GCACAGTGAG TGAACAGCTC 1020
 AGGAACTCAG AAACCAAGAA TCTGTGTCTC CTGGAAACAG CTCAATAA 1068

(3) INFORMATION FOR SEQ ID NO:2:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 355 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Asp Leu Glu Glu Thr Leu Phe Glu Glu Phe Glu Asn Tyr Ser
1 5 10 15

Tyr Asp Leu Asp Tyr Tyr Ser Leu Glu Ser Asp Leu Glu Glu Lys Val
20 25 30

30 Gln Leu Gly Val Val His Trp Val Ser Leu Val Leu Tyr Cys Leu Ala
35 40 45

Phe Val Leu Gly Ile Pro Gly Asn Ala Ile Val Ile Trp Phe Thr Gly
 50 55 60

Leu Lys Trp Lys Lys Thr Val Thr Thr Leu Trp Phe Leu Asn Leu Ala
 65 70 75 80

5 Ile Ala Asp Phe Ile Phe Leu Leu Phe Leu Pro Leu Tyr Ile Ser Tyr
 85 90 95

Val Ala Met Asn Phe His Trp Pro Phe Gly Ile Trp Leu Cys Lys Ala
 100 105 110

10 Asn Ser Phe Thr Ala Gln Leu Asn Met Phe Ala Ser Val Phe Phe Leu
 115 120 125

Thr Val Ile Ser Leu Asp His Tyr Ile His Leu Ile His Pro Val Leu
 130 135 140

Ser His Arg His Arg Thr Leu Lys Asn Ser Leu Ile Val Ile Ile Phe
 145 150 155 160

15 Ile Trp Leu Leu Ala Ser Leu Ile Gly Gly Pro Ala Leu Tyr Phe Arg
 165 170 175

Asp Thr Val Glu Phe Asn Asn His Thr Leu Cys Tyr Asn Asn Phe Gln
 180 185 190

20 Lys His Asp Pro Asp Leu Thr Leu Ile Arg His His Val Leu Thr Trp
 195 200 205

Val Lys Phe Ile Ile Gly Tyr Leu Phe Pro Leu Leu Thr Met Ser Ile
 210 215 220

Cys Tyr Leu Cys Leu Ile Phe Lys Val Lys Lys Arg Thr Val Leu Ile
 225 230 235 240

25 Ser Ser Arg His Phe Trp Thr Ile Leu Val Val Val Val Ala Phe Val
 245 250 255

Val Cys Trp Thr Pro Tyr His Leu Phe Ser Ile Trp Glu Leu Thr Ile
 260 265 270

30 His His Asn Ser Tyr Ser His His Val Met Gln Ala Gly Ile Pro Leu
 275 280 285

Ser Thr Gly Leu Ala Phe Leu Asn Ser Cys Leu Asn Pro Ile Leu Tyr
 290 295 300

Val Leu Ile Ser Lys Lys Phe Gln Ala Arg Phe Arg Ser Ser Val Ala
 305 310 315 320

35 Glu Ile Leu Lys Tyr Thr Leu Trp Glu Val Ser Cys Ser Gly Thr Val
 325 330 335

Ser Glu Gln Leu Arg Asn Ser Glu Thr Lys Asn Leu Cys Leu Leu Glu

340

345

350

Thr Ala Gln
355

(4) INFORMATION FOR SEQ ID NO:3:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1089 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- 10 (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGGCAACC ACACGTGGGA GGGCTGCCAC GTGGACTCGC GCGTGGACCA CCTCTTTCCG 60
CCATCCCTCT ACATCTTTGT CATCGGCGTG GGGCTGCCCA CCAACTGCCT GGCTCTGTGG 120
GCGGCCTACC GCCAGGTGCA ACAGCGCAAC GAGCTGGGCG TCTACCTGAT GAACCTCAGC 180
15 ATCGCCGACC TGCTGTACAT CTGCACGCTG CCGCTGTGGG TGGACTACTT CCTGCACCAC 240
GACAACTGGA TCCACGGCCC CGGGTCCTGC AAGCTCTTTG GGTTCATCTT CTACACCAAT 300
ATCTACATCA GCATCGCCTT CCTGTGCTGC ATCTCGGTGG ACCGCTACCT GGCTGTGGCC 360
CACCCACTCC GCTTCGCCCC CCTGCGCCGC GTCAAGACCG CCGTGGCCGT GAGCTCCGTG 420
GTCTGGGCCA CGGAGCTGGG CGCCAACTCG GCGCCCCTGT TCCATGACGA GCTCTTCCGA 480
20 GACCGCTACA ACCACACCTT CTGCTTTGAG AAGTTCCCCA TGGAAGGCTG GGTGGCCTGG 540
ATGAACCTCT ATCGGGTGTT CGTGGGCTTC CTCTTCCCGT GGGCGCTCAT GCTGCTGTCTG 600
TACCGGGGCA TCCTGCGGGC CGTGCGGGGC AGCGTGTTCA CCGAGCGCCA GGAGAAGGCC 660
AAGATCAAGC GGCTGGCCCT CAGCCTCATC GCCATCGTGC TGGTCTGCTT TCGGCCCTAT 720
CACGTGCTCT TGCTGTCCCG CAGCGCCATC TACCTGGGCC GCCCCTGGGA CTGCGGCTTC 780
25 GAGGAGCGCG TCTTTTCTGC ATACCACAGC TCACTGGCTT TCACCAGCCT CAACTGTGTG 840
GCGGACCCCA TCCTCTACTG CCTGGTCAAC GAGGGCGCCC GCAGCGATGT GGCCAAGGCC 900
CTGCACAACC TGCTCCGCTT TCTGGCCAGC GACAAGCCCC AGGAGATGGC CAATGCCTCG 960
CTCACCTTGG AGACCCCACT CACCTCCAAG AGGAACAGCA CAGCCAAAGC CATGACTGGC 1020
AGCTGGGCGG CCACTCCGCC TTCCAGGGG GACCAGGTGC AGCTGAAGAT GCTGCCGCCA 1080
30 GCACAATGA 1089

(5) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

10 Met Gly Asn His Thr Trp Glu Gly Cys His Val Asp Ser Arg Val Asp
 1 5 10 15
 His Leu Phe Pro Pro Ser Leu Tyr Ile Phe Val Ile Gly Val Gly Leu
 20 25 30
 Pro Thr Asn Cys Leu Ala Leu Trp Ala Ala Tyr Arg Gln Val Gln Gln
 35 40 45
 15 Arg Asn Glu Leu Gly Val Tyr Leu Met Asn Leu Ser Ile Ala Asp Leu
 50 55 60
 Leu Tyr Ile Cys Thr Leu Pro Leu Trp Val Asp Tyr Phe Leu His His
 65 70 75 80
 20 Asp Asn Trp Ile His Gly Pro Gly Ser Cys Lys Leu Phe Gly Phe Ile
 85 90 95
 Phe Tyr Thr Asn Ile Tyr Ile Ser Ile Ala Phe Leu Cys Cys Ile Ser
 100 105 110
 Val Asp Arg Tyr Leu Ala Val Ala His Pro Leu Arg Phe Ala Arg Leu
 115 120 125
 25 Arg Arg Val Lys Thr Ala Val Ala Val Ser Ser Val Val Trp Ala Thr
 130 135 140
 Glu Leu Gly Ala Asn Ser Ala Pro Leu Phe His Asp Glu Leu Phe Arg
 145 150 155 160
 30 Asp Arg Tyr Asn His Thr Phe Cys Phe Glu Lys Phe Pro Met Glu Gly
 165 170 175
 Trp Val Ala Trp Met Asn Leu Tyr Arg Val Phe Val Gly Phe Leu Phe
 180 185 190
 Pro Trp Ala Leu Met Leu Leu Ser Tyr Arg Gly Ile Leu Arg Ala Val
 195 200 205
 35 Arg Gly Ser Val Ser Thr Glu Arg Gln Glu Lys Ala Lys Ile Lys Arg
 210 215 220
 Leu Ala Leu Ser Leu Ile Ala Ile Val Leu Val Cys Phe Ala Pro Tyr

6

225 230 235 240
 His Val Leu Leu Leu Ser Arg Ser Ala Ile Tyr Leu Gly Arg Pro Trp
 245 250 255
 5 Asp Cys Gly Phe Glu Glu Arg Val Phe Ser Ala Tyr His Ser Ser Leu
 260 265 270
 Ala Phe Thr Ser Leu Asn Cys Val Ala Asp Pro Ile Leu Tyr Cys Leu
 275 280 285
 Val Asn Glu Gly Ala Arg Ser Asp Val Ala Lys Ala Leu His Asn Leu
 290 295 300
 10 Leu Arg Phe Leu Ala Ser Asp Lys Pro Gln Glu Met Ala Asn Ala Ser
 305 310 315 320
 Leu Thr Leu Glu Thr Pro Leu Thr Ser Lys Arg Asn Ser Thr Ala Lys
 325 330 335
 15 Ala Met Thr Gly Ser Trp Ala Ala Thr Pro Pro Ser Gln Gly Asp Gln
 340 345 350
 Val Gln Leu Lys Met Leu Pro Pro Ala Gln
 355 360

(6) INFORMATION FOR SEQ ID NO:5:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)

- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TATGAATTCA GATGCTCTAA ACGTCCCTGC

30

(7) INFORMATION FOR SEQ ID NO:6:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

35 TCCGGATCCA CCTGCACCTG CGCCTGCACC

30

(8) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1002 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGGAGTCCT CAGGCAACCC AGAGAGCACC ACCTTTTTTT ACTATGACCT TCAGAGCCAG 60
CCGTGTGAGA ACCAGGCCTG GGTCTTTGCT ACCCTCGCCA CCACTGTCCT GTACTGCCTG 120
10 GTGTTTCTCC TCAGCCTAGT GGGCAACAGC CTGGTCCTGT GGGTCCTGGT GAAGTATGAG 180
AGCCTGGAGT CCCTCACCAA CATCTTCATC CTCAACCTGT GCCTCTCAGA CCTGGTGTTC 240
GCCTGCTTGT TGCTGTGTG GATCTCCCCA TACCACTGGG GCTGGGTGCT GGGAGACTTC 300
CTCTGCAAAC TCCTCAATAT GATCTTCTCC ATCAGCCTCT ACAGCAGCAT CTTCTTCTCG 360
ACCATCATGA CCATCCACCG CTACCTGTCG GTAGTGAGCC CCCTCTCCAC CCTGCGCGTC 420
15 CCCACCCTCC GCTGCCGGGT GCTGGTGACC ATGGCTGTGT GGGTAGCCAG CATCCTGTCC 480
TCCATCCTCG ACACCATCTT CCACAAGGTG CTTTCTTCGG GCTGTGATTA TTCCGAAGTC 540
ACGTGGTACC TCACCTCCGT CTACCAGCAC AACCTCTTCT TCCTGCTGTC CCTGGGGATT 600
ATCCTGTTCT GCTACGTGGA GATCCTCAGG ACCCTGTTCC GCTCACGCTC CAAGCGGCGC 660
CACCGCACGG TCAAGCTCAT CTTGCCATC GTGGTGGCCT ACTTCCTCAG CTGGGGTCCC 720
20 TACAACTTCA CCCTGTTTCT GCAGACGCTG TTTCGGACCC AGATCATCCG GAGCTGCGAG 780
GCCAAACAGC AGCTAGAATA CGCCCTGCTC ATCTGCCGCA ACCTCGCCTT CTCCCACTGC 840
TGCTTTAACC CGGTGCTCTA TGTCTTCGTG GGGGTCAAGT TCCGCACACA CCTGAAACAT 900
GTTCTCCGGC AGTTCTGGTT CTGCCGGCTG CAGGCACCCA GCCCAGCCTC GATCCCCCAC 960
TCCCCTGGTG CCTTCGCCTA TGAGGGCGCC TCCTTCTACT GA 1002

25 (9) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Glu Ser Ser Gly Asn Pro Glu Ser Thr Thr Phe Phe Tyr Tyr Asp
 1 5 10 15
 Leu Gln Ser Gln Pro Cys Glu Asn Gln Ala Trp Val Phe Ala Thr Leu
 20 25 30
 5 Ala Thr Thr Val Leu Tyr Cys Leu Val Phe Leu Leu Ser Leu Val Gly
 35 40 45
 Asn Ser Leu Val Leu Trp Val Leu Val Lys Tyr Glu Ser Leu Glu Ser
 50 55 60
 10 Leu Thr Asn Ile Phe Ile Leu Asn Leu Cys Leu Ser Asp Leu Val Phe
 65 70 75 80
 Ala Cys Leu Leu Pro Val Trp Ile Ser Pro Tyr His Trp Gly Trp Val
 85 90 95
 Leu Gly Asp Phe Leu Cys Lys Leu Leu Asn Met Ile Phe Ser Ile Ser
 100 105 110
 15 Leu Tyr Ser Ser Ile Phe Phe Leu Thr Ile Met Thr Ile His Arg Tyr
 115 120 125
 Leu Ser Val Val Ser Pro Leu Ser Thr Leu Arg Val Pro Thr Leu Arg
 130 135 140
 20 Cys Arg Val Leu Val Thr Met Ala Val Trp Val Ala Ser Ile Leu Ser
 145 150 155 160
 Ser Ile Leu Asp Thr Ile Phe His Lys Val Leu Ser Ser Gly Cys Asp
 165 170 175
 Tyr Ser Glu Leu Thr Trp Tyr Leu Thr Ser Val Tyr Gln His Asn Leu
 180 185 190
 25 Phe Phe Leu Leu Ser Leu Gly Ile Ile Leu Phe Cys Tyr Val Glu Ile
 195 200 205
 Leu Arg Thr Leu Phe Arg Ser Arg Ser Lys Arg Arg His Arg Thr Val
 210 215 220
 30 Lys Leu Ile Phe Ala Ile Val Val Ala Tyr Phe Leu Ser Trp Gly Pro
 225 230 235 240
 Tyr Asn Phe Thr Leu Phe Leu Gln Thr Leu Phe Arg Thr Gln Ile Ile
 245 250 255
 Arg Ser Cys Glu Ala Lys Gln Gln Leu Glu Tyr Ala Leu Leu Ile Cys
 260 265 270
 35 Arg Asn Leu Ala Phe Ser His Cys Cys Phe Asn Pro Val Leu Tyr Val
 275 280 285

Phe Val Gly Val Lys Phe Arg Thr His Leu Lys His Val Leu Arg Gln
290 295 300

Phe Trp Phe Cys Arg Leu Gln Ala Pro Ser Pro Ala Ser Ile Pro His
305 310 315 320

5 Ser Pro Gly Ala Phe Ala Tyr Glu Gly Ala Ser Phe Tyr
325 330

(10) INFORMATION FOR SEQ ID NO:9:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

15 GCAAGCTTGG GGGACGCCAG GTCGCCGGCT 30

(11) INFORMATION FOR SEQ ID NO:10:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCGGATCCGG ACGCTGGGGG AGTCAGGCTG C 31

25 (12) INFORMATION FOR SEQ ID NO:11:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 987 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGGACAACG CCTCGTTCTC GGAGCCCTGG CCCGCCAACG CATCGGGCCC GGACCCGGCG 60

CTGAGCTGCT CCAACGCGTC GACTCTGGCG CCGCTGCCGG CGCCGCTGGC GGTGGCTGTA 120

35 CCAATTGTCT ACGCGGTGAT CTGCGCCGTG GGTCTGGCGG GCAACTCCGC CGTGCTGTAC 180

GTGTTGCTGC GGGCGCCCCG CATGAAGACC GTCACCAACC TGTTCATCCT CAACCTGGCC 240
 ATCGCCGACG AGCTCTTCAC GCTGGTGCTG CCCATCAACA TCGCCGACTT CCTGTGCGG 300
 CAGTGGCCCT TCGGGGAGCT CATGTGCAAG CTCATCGTGG CTATCGACCA GTACAACACC 360
 TTCTCCAGCC TCTACTTCCT CACCGTCATG AGCGCCGACC GCTACCTGGT GGTGTTGGCC 420
 5 ACTGCGGAGT CGCGCCGGGT GGCCGGCCGC ACCTACAGCG CCGCGCGCGC GGTGAGCCTG 480
 GCCGTGTGGG GGATCGTCAC ACTCGTCGTG CTGCCCTTCG CAGTCTTCGC CCGGCTAGAC 540
 GACGAGCAGG GCCGGCGCCA GTGCGTGCTA GTCTTTCCGC AGCCCGAGGC CTTCTGGTGG 600
 CGCGCGAGCC GCCTCTACAC GCTCGTGCTG GGCTTCGCCA TCCCCGTGTC CACCATCTGT 660
 GTCCTCTATA CCACCCTGCT GTGCCGGCTG CATGCCATGC GGCTGGACAG CCACGCCAAG 720
 10 GCCCTGGAGC GCGCEAAGAA GCGGGTGACC TTCCTGGTGG TGGCAATCCT GGCGGTGTGC 780
 CTCCTCTGCT GGACGCCCTA CCACCTGAGC ACCGTGGTGG CGCTCACCAC CGACCTCCCCG 840
 CAGACGCCGC TGGTCATCGC TATCTCCTAC TTCATCACCA GCCTGACGTA CGCCAACAGC 900
 TGCCTCAACC CCTTCCTCTA CGCCTTCCTG GACGCCAGCT TCCGCAGGAA CCTCCGCCAG 960
 CTGATAACTT GCCGCGCGGC AGCCTGA 987

15 (13) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 328 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant

20

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Asp Asn Ala Ser Phe Ser Glu Pro Trp Pro Ala Asn Ala Ser Gly
 1 5 10 15
 25 Pro Asp Pro Ala Leu Ser Cys Ser Asn Ala Ser Thr Leu Ala Pro Leu
 20 25 30
 Pro Ala Pro Leu Ala Val Ala Val Pro Val Val Tyr Ala Val Ile Cys
 35 40 45
 30 Ala Val Gly Leu Ala Gly Asn Ser Ala Val Leu Tyr Val Leu Leu Arg
 50 55 60
 Ala Pro Arg Met Lys Thr Val Thr Asn Leu Phe Ile Leu Asn Leu Ala
 65 70 75 80

11

	Ile	Ala	Asp	Glu	Leu	Phe	Thr	Leu	Val	Leu	Pro	Ile	Asn	Ile	Ala	Asp	
					85					90					95		
	Phe	Leu	Leu	Arg	Gln	Trp	Pro	Phe	Gly	Glu	Leu	Met	Cys	Lys	Leu	Ile	
				100					105					110			
5	Val	Ala	Ile	Asp	Gln	Tyr	Asn	Thr	Phe	Ser	Ser	Leu	Tyr	Phe	Leu	Thr	
			115					120					125				
	Val	Met	Ser	Ala	Asp	Arg	Tyr	Leu	Val	Val	Leu	Ala	Thr	Ala	Glu	Ser	
		130					135					140					
10	Arg	Arg	Val	Ala	Gly	Arg	Thr	Tyr	Ser	Ala	Ala	Arg	Ala	Val	Ser	Leu	
	145					150					155					160	
	Ala	Val	Trp	Gly	Ile	Val	Thr	Leu	Val	Val	Leu	Pro	Phe	Ala	Val	Phe	
				165						170					175		
	Ala	Arg	Leu	Asp	Asp	Glu	Gln	Gly	Arg	Arg	Gln	Cys	Val	Leu	Val	Phe	
				180					185					190			
15	Pro	Gln	Pro	Glu	Ala	Phe	Trp	Trp	Arg	Ala	Ser	Arg	Leu	Tyr	Thr	Leu	
			195					200					205				
	Val	Leu	Gly	Phe	Ala	Ile	Pro	Val	Ser	Thr	Ile	Cys	Val	Leu	Tyr	Thr	
		210					215					220					
20	Thr	Leu	Leu	Cys	Arg	Leu	His	Ala	Met	Arg	Leu	Asp	Ser	His	Ala	Lys	
	225					230					235					240	
	Ala	Leu	Glu	Arg	Ala	Lys	Lys	Arg	Val	Thr	Phe	Leu	Val	Val	Ala	Ile	
				245						250					255		
	Leu	Ala	Val	Cys	Leu	Leu	Cys	Trp	Thr	Pro	Tyr	His	Leu	Ser	Thr	Val	
			260					265						270			
25	Val	Ala	Leu	Thr	Thr	Asp	Leu	Pro	Gln	Thr	Pro	Leu	Val	Ile	Ala	Ile	
			275				280						285				
	Ser	Tyr	Phe	Ile	Thr	Ser	Leu	Thr	Tyr	Ala	Asn	Ser	Cys	Leu	Asn	Pro	
		290					295					300					
30	Phe	Leu	Tyr	Ala	Phe	Leu	Asp	Ala	Ser	Phe	Arg	Arg	Asn	Leu	Arg	Gln	
	305					310					315					320	
	Leu	Ile	Thr	Cys	Arg	Ala	Ala	Ala									
						325											

(14) INFORMATION FOR SEQ ID NO:13:

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CGGAATTCGT CAACGGTCCC AGCTACAATG

30

(15) INFORMATION FOR SEQ ID NO:14:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- 10 (ii) MOLECULE TYPE: DNA (genomic)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATGGATCCCA GGCCCTTCAG CACCGCAATA T

31

(16) INFORMATION FOR SEQ ID NO:15:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1002 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATGCAGGCCG CTGGGCACCC AGAGCCCCTT GACAGCAGGG GCTCCTTCTC CCTCCCCACG 60

ATGGGTGCCA ACGTCTCTCA GGACAATGGC ACTGGCCACA ATGCCACCTT CTCCGAGCCA 120

CTGCCGTTCC TCTATGTGCT CCTGCCCCGCC GTGTACTCCG GGATCTGTGC TGTGGGGCTG 180

ACTGGCAACA CGGCCGTCAT CTTGTAATC CTAAGGGCGC CCAAGATGAA GACGGTGACC 240

- 25 AACGTGTTCA TCCTGAACCT GGCCGTCGCC GACGGGCTCT TCACGCTGGT ACTGCCCCGTC 300

AACATCGCGG AGCACCTGCT GCAGTACTGG CCCTTCGGGG AGCTGCTCTG CAAGCTGGTG 360

CTGGCCGTCG ACCACTACAA CATCTTCTCC AGCATCTACT TCCTAGCCGT GATGAGCGTG 420

GACCGATAACC TGGTGGTGCT GGCCACCGTG AGGTCCCGCC ACATGCCCTG GCGCACCTAC 480

CGGGGGGCGA AGGTCGCCAG CCTGTGTGTC TGGCTGGGCG TCACGGTCCT GGTCTGCCCC 540

- 30 TTCTTCTCTT TCGCTGGCGT CTACAGCAAC GAGCTGCAGG TCCAAGCTG TGGGCTGAGC 600

TTCCCGTGGC CCGAGCGGGT CTGGTTCAAG GCCAGCCGTG TCTACACTTT GGTCTGGGGC 660

TTCGTGCTGC CCGTGTGCAC CATCTGTGTG CTCTACACAG ACCTCCTGCG CAGGCTGCGG 720

GCCGTGCGGC TCCGCTCTGG AGCCAAGGCT CTAGGCAAGG CCAGGCGGAA GGTGACCGTC 780
 CTGGTCCTCG TCGTGCTGGC CGTGTGCCTC CTCTGCTGGA CGCCCTTCCA CCTGGCCTCT 840
 GTCGTGGCCC TGACCACGGA CCTGCCCCAG ACCCCACTGG TCATCAGTAT GTCCTACGTC 900
 ATCACCAGCC TCACGTACGC CAACTCGTGC CTGAACCCCT TCCTCTACGC CTTTCTAGAT 960
 5 GACAACTTCC GGAAGAACTT CCGCAGCATA TTGCGGTGCT GA 1002

(17) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 333 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

15 Met Gln Ala Ala Gly His Pro Glu Pro Leu Asp Ser Arg Gly Ser Phe
 1 5 10 15
 Ser Leu Pro Thr Met Gly Ala Asn Val Ser Gln Asp Asn Gly Thr Gly
 20 20 25 30
 His Asn Ala Thr Phe Ser Glu Pro Leu Pro Phe Leu Tyr Val Leu Leu
 35 40 45
 20 Pro Ala Val Tyr Ser Gly Ile Cys Ala Val Gly Leu Thr Gly Asn Thr
 50 55 60
 Ala Val Ile Leu Val Ile Leu Arg Ala Pro Lys Met Lys Thr Val Thr
 65 70 75 80
 25 Asn Val Phe Ile Leu Asn Leu Ala Val Ala Asp Gly Leu Phe Thr Leu
 85 90 95
 Val Leu Pro Val Asn Ile Ala Glu His Leu Leu Gln Tyr Trp Pro Phe
 100 105 110
 Gly Glu Leu Leu Cys Lys Leu Val Leu Ala Val Asp His Tyr Asn Ile
 115 120 125
 30 Phe Ser Ser Ile Tyr Phe Leu Ala Val Met Ser Val Asp Arg Tyr Leu
 130 135 140
 Val Val Leu Ala Thr Val Arg Ser Arg His Met Pro Trp Arg Thr Tyr
 145 150 155 160
 35 Arg Gly Ala Lys Val Ala Ser Leu Cys Val Trp Leu Gly Val Thr Val
 165 170 175

14

Leu Val Leu Pro Phe Phe Ser Phe Ala Gly Val Tyr Ser Asn Glu Leu
 180 185 190
 Gln Val Pro Ser Cys Gly Leu Ser Phe Pro Trp Pro Glu Arg Val Trp
 195 200 205
 5 Phe Lys Ala Ser Arg Val Tyr Thr Leu Val Leu Gly Phe Val Leu Pro
 210 215 220
 Val Cys Thr Ile Cys Val Leu Tyr Thr Asp Leu Leu Arg Arg Leu Arg
 225 230 235 240
 10 Ala Val Arg Leu Arg Ser Gly Ala Lys Ala Leu Gly Lys Ala Arg Arg
 245 250 255
 Lys Val Thr Val Leu Val Leu Val Val Leu Ala Val Cys Leu Leu Cys
 260 265 270
 Trp Thr Pro Phe His Leu Ala Ser Val Val Ala Leu Thr Thr Asp Leu
 275 280 285
 15 Pro Gln Thr Pro Leu Val Ile Ser Met Ser Tyr Val Ile Thr Ser Leu
 290 295 300
 Thr Tyr Ala Asn Ser Cys Leu Asn Pro Phe Leu Tyr Ala Phe Leu Asp
 305 310 315 320
 20 Asp Asn Phe Arg Lys Asn Phe Arg Ser Ile Leu Arg Cys
 325 330

(18) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 48 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ACGAATTCAG CCATGGTCCT TGAGGTGAGT GACCACCAAG TGCTAAAT

48

30 (19) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 35 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GAGGATCCTG GAATGCGGGG AAGTCAG

27

(20) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1107 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

10 ATGGTCCTTG AGGTGAGTGA CCACCAAGTG CTAAATGACG CCGAGGTTGC CGCCCTCCTG 60
GAGAACTTCA GCTCTTCTTA TGACTATGGA GAAAACGAGA GTGACTCGTG CTGTACCTCC 120
CCGCCCTGCC CACAGGACTT CAGCCTGAAC TTCGACCGGG CCTTCCTGCC AGCCCTCTAC 180
AGCCTCCTCT TTCTGCTGGG GCTGCTGGGC AACGGCGCGG TGGCAGCCGT GCTGCTGAGC 240
CGGCGGACAG CCCTGAGCAG CACCGACACC TTCCTGCTCC ACCTAGCTGT AGCAGACACG 300
15 CTGCTGGTGC TGACACTGCC GCTCTGGGCA GTGGACGCTG CCGTCCAGTG GGTCTTTGGC 360
TCTGGCCTCT GCAAAGTGGC AGGTGCCCTC TTCAACATCA ACTTCTACGC AGGAGCCCTC 420
CTGCTGGCCT GCATCAGCTT TGACCGCTAC CTGAACATAG TTCATGCCAC CCAGCTCTAC 480
CGCCGGGGGC CCCC GGCCCG CGTGACCCTC ACCTGCCTGG CTGTCTGGGG GCTCTGCCTG 540
CTTTTCGCCC TCCCAGACTT CATCTTCCTG TCGGCCACC ACGACGAGCG CCTCAACGCC 600
20 ACCCACTGCC AATACAATT CCCACAGGTG GGCCGCACGG CTCTGCGGGT GCTGCAGCTG 660
GTGGCTGGCT TTCTGCTGCC CCTGCTGGTC ATGGCCTACT GCTATGCCCA CATCCTGGCC 720
GTGCTGCTGG TTTCCAGGGG CCAGCGGCGC CTGCGGGCCA TGC GGCTGGT GGTGGTGGTC 780
GTGGTGGCCT TTGCCCTCTG CTGGACCCCT TATCACCTGG TGGTGTGGT GGACATCCTC 840
ATGGACCTGG GCGCTTTGGC CCGCAACTGT GGCCGAGAAA GCAGGGTAGA CGTGGCCAAG 900
25 TCGGTCACCT CAGGCCTGGG CTACATGCAC TGCTGCCTCA ACCCGCTGCT CTATGCCTTT 960
GTAGGGGTCA AGTTCCGGGA GCGGATGTGG ATGCTGCTCT TGC GCCTGGG CTGCCCCAAC 1020
CAGAGAGGGC TCCAGAGGCA GCCATCGTCT TCCCGCCGGG ATTCATCCTG GTCTGAGACC 1080
TCAGAGGCCT CCTACTCGGG CTGTGA 1107

(21) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 368 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

5

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

	Met	Val	Leu	Glu	Val	Ser	Asp	His	Gln	Val	Leu	Asn	Asp	Ala	Glu	Val	
	1				5					10					15		
10	Ala	Ala	Leu	Leu	Glu	Asn	Phe	Ser	Ser	Ser	Tyr	Asp	Tyr	Gly	Glu	Asn	
			20						25					30			
	Glu	Ser	Asp	Ser	Cys	Cys	Thr	Ser	Pro	Pro	Cys	Pro	Gln	Asp	Phe	Ser	
			35					40					45				
15	Leu	Asn	Phe	Asp	Arg	Ala	Phe	Leu	Pro	Ala	Leu	Tyr	Ser	Leu	Leu	Phe	
		50					55					60					
	Leu	Leu	Gly	Leu	Leu	Gly	Asn	Gly	Ala	Val	Ala	Ala	Val	Leu	Leu	Ser	
		65				70				75					80		
	Arg	Arg	Thr	Ala	Leu	Ser	Ser	Thr	Asp	Thr	Phe	Leu	Leu	His	Leu	Ala	
					85					90					95		
20	Val	Ala	Asp	Thr	Leu	Leu	Val	Leu	Thr	Leu	Pro	Leu	Trp	Ala	Val	Asp	
				100					105					110			
	Ala	Ala	Val	Gln	Trp	Val	Phe	Gly	Ser	Gly	Leu	Cys	Lys	Val	Ala	Gly	
			115					120					125				
25	Ala	Leu	Phe	Asn	Ile	Asn	Phe	Tyr	Ala	Gly	Ala	Leu	Leu	Leu	Ala	Cys	
		130					135					140					
	Ile	Ser	Phe	Asp	Arg	Tyr	Leu	Asn	Ile	Val	His	Ala	Thr	Gln	Leu	Tyr	
		145				150					155				160		
	Arg	Arg	Gly	Pro	Pro	Ala	Arg	Val	Thr	Leu	Thr	Cys	Leu	Ala	Val	Trp	
				165					170					175			
30	Gly	Leu	Cys	Leu	Leu	Phe	Ala	Leu	Pro	Asp	Phe	Ile	Phe	Leu	Ser	Ala	
				180					185					190			
	His	His	Asp	Glu	Arg	Leu	Asn	Ala	Thr	His	Cys	Gln	Tyr	Asn	Phe	Pro	
			195					200					205				
35	Gln	Val	Gly	Arg	Thr	Ala	Leu	Arg	Val	Leu	Gln	Leu	Val	Ala	Gly	Phe	
			210				215					220					
	Leu	Leu	Pro	Leu	Leu	Val	Met	Ala	Tyr	Cys	Tyr	Ala	His	Ile	Leu	Ala	
		225				230					235				240		

	Val	Leu	Leu	Val	Ser	Arg	Gly	Gln	Arg	Arg	Leu	Arg	Ala	Met	Arg	Leu	
					245					250					255		
	Val	Val	Val	Val	Val	Val	Ala	Phe	Ala	Leu	Cys	Trp	Thr	Pro	Tyr	His	
				260					265					270			
5	Leu	Val	Val	Leu	Val	Asp	Ile	Leu	Met	Asp	Leu	Gly	Ala	Leu	Ala	Arg	
			275					280					285				
	Asn	Cys	Gly	Arg	Glu	Ser	Arg	Val	Asp	Val	Ala	Lys	Ser	Val	Thr	Ser	
		290					295					300					
10	Gly	Leu	Gly	Tyr	Met	His	Cys	Cys	Leu	Asn	Pro	Leu	Leu	Tyr	Ala	Phe	
	305					310					315					320	
	Val	Gly	Val	Lys	Phe	Arg	Glu	Arg	Met	Trp	Met	Leu	Leu	Leu	Arg	Leu	
					325					330					335		
	Gly	Cys	Pro	Asn	Gln	Arg	Gly	Leu	Gln	Arg	Gln	Pro	Ser	Ser	Ser	Arg	
				340					345					350			
15	Arg	Asp	Ser	Ser	Trp	Ser	Glu	Thr	Ser	Glu	Ala	Ser	Tyr	Ser	Gly	Leu	
			355					360					365				

(22) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

25 TTAAGCTTGA CCTAATGCCA TCTTGTGTCC 30

(23) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TTGGATCCAA AAGAACCATG CACCTCAGAG 30

35 (24) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1074 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

```
ATGGCTGATG ACTATGGCTC TGAATCCACA TCTTCCATGG AAGACTACGT TAACTTCAAC 60
TTCAGTGAAT TCTACTGTGA GAAAAACAAT GTCAGGCAGT TTGCGAGCCA TTTCTCTCCA 120
CCCTTGTAAT GGCTCGTGTT CATCGTGGGT GCCTTGGGCA ACAGTCTTGT TATCCTTGTC 180
10 TACTGGTACT GCACAAGAGT GAAGACCATG ACCGACATGT TCCTTTTGAA TTTGGCAATT 240
GCTGACCTCC TCTTTCTTGT CACTCTTCCC TTCTGGGCCA TTGCTGCTGC TGACCAGTGG 300
AAGTTCCAGA CCTTCATGTG CAAGGTGGTC AACAGCATGT ACAAGATGAA CTCTACAGC 360
TGTGTGTTGC TGATCATGTG CATCAGCGTG GACAGGTACA TTGCCATTGC CCAGGCCATG 420
AGAGCACATA CTTGGAGGGA GAAAAGGCTT TTGTACAGCA AAATGGTTTG CTTTACCATC 480
15 TGGGTATTGG CAGCTGCTCT CTGCATCCCA GAAATCTTAT ACAGCCAAAT CAAGGAGGAA 540
TCCGGCATTG CTATCTGCAC CATGGTTTAC CCTAGCGATG AGAGCACCAA ACTGAAGTCA 600
GCTGTCTTGA CCCTGAAGGT CATTCTGGGG TTCTTCCTTC CCTTCGTGGT CATGGCTTGC 660
TGCTATACCA TCATCATTCA CACCCTGATA CAAGCCAAGA AGTCTTCCAA GCACAAAGCC 720
CTAAAAGTGA CCATCACTGT CCTGACCGTC TTTGTCTTGT CTCAGTTTCC CTACAACTGC 780
20 ATTTTGTGGG TGCAGACCAT TGACGCCTAT GCCATGTTCA TCTCCAACG TGCCGTTTCC 840
ACCAACATTG ACATCTGCTT CCAGGTCACC CAGACCATCG CCTTCTTCCA CAGTTGCCTG 900
AACCCTGTTT TCTATGTTTT TGTGGGTGAG AGATTCCGCC GGGATCTCGT GAAAACCCTG 960
AAGAACTTGG GTTGCATCAG CCAGGCCAG TGGGTTTCAT TTACAAGGAG AGAGGGAAGC 1020
TTGAAGCTGT CGTCTATGTT GCTGGAGACA ACCTCAGGAG CACTCTCCCT CTGA 1074
```

25 (25) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 357 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant

30

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

	Met	Ala	Asp	Asp	Tyr	Gly	Ser	Glu	Ser	Thr	Ser	Ser	Met	Glu	Asp	Tyr	
	1				5					10					15		
5	Val	Asn	Phe	Asn	Phe	Thr	Asp	Phe	Tyr	Cys	Glu	Lys	Asn	Asn	Val	Arg	
				20					25					30			
	Gln	Phe	Ala	Ser	His	Phe	Leu	Pro	Pro	Leu	Tyr	Trp	Leu	Val	Phe	Ile	
			35					40						45			
	Val	Gly	Ala	Leu	Gly	Asn	Ser	Leu	Val	Ile	Leu	Val	Tyr	Trp	Tyr	Cys	
		50					55					60					
10	Thr	Arg	Val	Lys	Thr	Met	Thr	Asp	Met	Phe	Leu	Leu	Asn	Leu	Ala	Ile	
	65					70					75					80	
	Ala	Asp	Leu	Leu	Phe	Leu	Val	Thr	Leu	Pro	Phe	Trp	Ala	Ile	Ala	Ala	
					85					90					95		
15	Ala	Asp	Gln	Trp	Lys	Phe	Gln	Thr	Phe	Met	Cys	Lys	Val	Val	Asn	Ser	
				100					105						110		
	Met	Tyr	Lys	Met	Asn	Phe	Tyr	Ser	Cys	Val	Leu	Leu	Ile	Met	Cys	Ile	
			115					120					125				
	Ser	Val	Asp	Arg	Tyr	Ile	Ala	Ile	Ala	Gln	Ala	Met	Arg	Ala	His	Thr	
		130					135					140					
20	Trp	Arg	Glu	Lys	Arg	Leu	Leu	Tyr	Ser	Lys	Met	Val	Cys	Phe	Thr	Ile	
	145					150					155					160	
	Trp	Val	Leu	Ala	Ala	Ala	Leu	Cys	Ile	Pro	Glu	Ile	Leu	Tyr	Ser	Gln	
				165						170					175		
25	Ile	Lys	Glu	Glu	Ser	Gly	Ile	Ala	Ile	Cys	Thr	Met	Val	Tyr	Pro	Ser	
			180						185					190			
	Asp	Glu	Ser	Thr	Lys	Leu	Lys	Ser	Ala	Val	Leu	Thr	Leu	Lys	Val	Ile	
			195					200					205				
	Leu	Gly	Phe	Phe	Leu	Pro	Phe	Val	Val	Met	Ala	Cys	Cys	Tyr	Thr	Ile	
		210					215					220					
30	Ile	Ile	His	Thr	Leu	Ile	Gln	Ala	Lys	Lys	Ser	Ser	Lys	His	Lys	Ala	
	225				230					235						240	
	Leu	Lys	Val	Thr	Ile	Thr	Val	Leu	Thr	Val	Phe	Val	Leu	Ser	Gln	Phe	
				245						250					255		
35	Pro	Tyr	Asn	Cys	Ile	Leu	Leu	Val	Gln	Thr	Ile	Asp	Ala	Tyr	Ala	Met	
			260					265						270			
	Phe	Ile	Ser	Asn	Cys	Ala	Val	Ser	Thr	Asn	Ile	Asp	Ile	Cys	Phe	Gln	
			275					280					285				

20

Val Thr Gln Thr Ile Ala Phe Phe His Ser Cys Leu Asn Pro Val Leu
290 295 300

Tyr Val Phe Val Gly Glu Arg Phe Arg Arg Asp Leu Val Lys Thr Leu
305 310 315 320

5 Lys Asn Leu Gly Cys Ile Ser Gln Ala Gln Trp Val Ser Phe Thr Arg
325 330 335

Arg Glu Gly Ser Leu Lys Leu Ser Ser Met Leu Leu Glu Thr Thr Ser
340 345 350

10 Gly Ala Leu Ser Leu
355

(26) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1110 base pairs.
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATGGCCTCAT CGACCACTCG GGGCCCCAGG GTTCTGACT TATTTTCTGG GCTGCCGCCG 60

20 GCGGTCACAA CTCCCGCCAA CCAGAGCGCA GAGGCCTCGG CGGGCAACGG GTCGGTGGCT 120

GGCGCGGACG CTCCAGCCGT CACGCCCTTC CAGAGCCTGC AGCTGGTGCA TCAGCTGAAG 180

GGGCTGATCG TGCTGCTCTA CAGCGTCGTG GTGGTCGTGG GGCTGGTGGG CAACTGCCTG 240

CTGGTGCTGG TGATCGCGCG GGTGCCGCGG CTGCACAACG TGACGAACTT CCTCATCGGC 300

AACCTGGCCT TGTCGACGT GTCATGTGC ACCGCCTGCG TGCCGCTCAC GCTGGCCTAT 360

25 GCCTTCGAGC CACGCGGCTG GGTGTTCCGC GCGGCCTGT GCCACCTGGT CTTCTTCCTG 420

CAGCCGGTCA CCGTCTATGT GTCGGTGTTT ACGCTACCA CCATCGCAGT GGACCGCTAC 480

GTCGTGCTGG TGACCCGCT GAGGCGCGCA TCTCGCTGCG CCTCAGCCTA CGCTGTGCTG 540

GCCATCTGGG CGCTGTCCGC GGTGCTGGCG CTGCCGCCCG CCGTGACAC CTATCACGTG 600

GAGCTCAAGC CGCAGACGT GCGCCTCTGC GAGGAGTTCT GGGGCTCCCA GGAGCGCCAG 660

30 CGCCAGCTCT ACGCCTGGGG GCTGCTGCTG GTCACCTACC TGCTCCCTCT GCTGGTCATC 720

CTCCTGTCTT ACGTCCGGGT GTCAGTGAAG CTCCGCAACC GCGTGGTGCC GGGCTGCGTG 780

ACCCAGAGCC AGGCCGACTG GGACCGCGCT CGGCGCCGGC GCACCTTCTG CTTGCTGGTG 840

GTGGTCGTGG TGGTGTTCGC CGTCTGCTGG CTGCCGCTGC ACGTCTTCAA CCTGCTGCGG 900
 GACCTCGACC CCCACGCCAT CGACCCTTAC GCCTTTGGGC TGGTGCAGCT GCTCTGCCAC 960
 TGGCTCGCCA TGAGTTCGGC CTGCTACAAC CCCTTCATCT ACGCCTGGCT GCACGACAGC 1020
 TTCCGCGAGG AGCTGCGCAA ACTGTTGGTC GCTTGGCCCC GCAAGATAGC CCCCCATGGC 1080
 5 CAGAATATGA CCGTCAGCGT GGTCATCTGA 1110

(27) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 369 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

15 Met Ala Ser Ser Thr Thr Arg Gly Pro Arg Val Ser Asp Leu Phe Ser
 1 5 10 15
 Gly Leu Pro Pro Ala Val Thr Thr Pro Ala Asn Gln Ser Ala Glu Ala
 20 25 30
 Ser Ala Gly Asn Gly Ser Val Ala Gly Ala Asp Ala Pro Ala Val Thr
 35 40 45
 20 Pro Phe Gln Ser Leu Gln Leu Val His Gln Leu Lys Gly Leu Ile Val
 50 55 60
 Leu Leu Tyr Ser Val Val Val Val Val Gly Leu Val Gly Asn Cys Leu
 65 70 75 80
 25 Leu Val Leu Val Ile Ala Arg Val Pro Arg Leu His Asn Val Thr Asn
 85 90 95
 Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu Met Cys Thr Ala
 100 105 110
 Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly Trp Val
 115 120 125
 30 Phe Gly Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Pro Val Thr
 130 135 140
 Val Tyr Val Ser Val Phe Thr Leu Thr Thr Ile Ala Val Asp Arg Tyr
 145 150 155 160
 35 Val Val Leu Val His Pro Leu Arg Arg Ala Ser Arg Cys Ala Ser Ala
 165 170 175

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Tyr Ala Val Leu Ala Ile Trp Ala Leu Ser Ala Val Leu Ala Leu Pro
 180 185 190
 Pro Ala Val His Thr Tyr His Val Glu Leu Lys Pro His Asp Val Arg
 195 200 205
 5 Leu Cys Glu Glu Phe Trp Gly Ser Gln Glu Arg Gln Arg Gln Leu Tyr
 210 215 220
 Ala Trp Gly Leu Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val Ile
 225 230 235 240
 10 Leu Leu Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg Val Val
 245 250 255
 Pro Gly Cys Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg Arg
 260 265 270
 Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Val Phe Ala Val
 275 280 285
 15 Cys Trp Leu Pro Leu His Val Phe Asn Leu Leu Arg Asp Leu Asp Pro
 290 295 300
 His Ala Ile Asp Pro Tyr Ala Phe Gly Leu Val Gln Leu Leu Cys His
 305 310 315 320
 20 Trp Leu Ala Met Ser Ser Ala Cys Tyr Asn Pro Phe Ile Tyr Ala Trp
 325 330 335
 Leu His Asp Ser Phe Arg Glu Glu Leu Arg Lys Leu Leu Val Ala Trp
 340 345 350
 Pro Arg Lys Ile Ala Pro His Gly Gln Asn Met Thr Val Ser Val Val
 355 360 365
 25 Ile

(28) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1083 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:
 35 ATGGACCCAG AAGAACTTC AGTTTATTTG GATTATTACT ATGCTACGAG CCCAACTCT 60
 GACATCAGGG AGACCCACTC CCATGTTCTT TACACCTCTG TCTTCCTTCC AGTCTTTTAC 120

ACAGCTGTGT TCCTGACTGG AGTGCTGGGG AACCTTGTTT TCATGGGAGC GTTGCATTTT 180
 AAACCCGGCA GCCGAAGACT GATCGACATC TTTATCATCA ATCTGGCTGC CTCTGACTTC 240
 ATTTTCTTGT TCACATTGCC TCTCTGGGTG GATAAAGAAG CATCTCTAGG ACTGTGGAGG 300
 ACGGGCTCCT TCCTGTGCAA AGGGAGCTCC TACATGATCT CCGTCAATAT GCACTGCAGT 360
 5 GTCCTCCTGC TCACTTGCAAT GAGTGTGAC CGCTACCTGG CCATTGTGTG GCCAGTCGTA 420
 TCCAGGAAAT TCAGAAGGAC AGACTGTGCA TATGTAGTCT GTGCCAGCAT CTGGTTTATC 480
 TCCTGCCTGC TGGGGTTGCC TACTCTTCTG TCCAGGGAGC TCACGCTGAT TGATGATAAG 540
 CCATACTGTG CAGAGAAAAA GGCAACTCCA ATTAACTCA TATGGTCCCT GGTGGCCTTA 600
 ATTTTCACCT TTTTGTCCC TTTGTTGAGC ATTGTGACCT GCTACTGTTG CATTGCAAGG 660
 10 AAGCTGTGTG CCCATTACCA GCAATCAGGA AAGCACAACA AAAAGCTGAA GAAATCTATA 720
 AAGATCATCT TTATTGTCGT GGCAGCCTTT CTTGTCTCCT GGCTGCCCTT CAATACTTTT 780
 AAGTTCCTGG CCATTGTCTC TGGGTTGCGG CAAGAACACT ATTTACCCTC AGCTATTCTT 840
 CAGCTTGTA TGGAGGTGAG TGGACCCTTG GCATTGCGCA ACAGCTGTGT CAACCCTTTT 900
 ATTTACTATA TCTTCGACAG CTACATCCGC CGGGCCATTG TCCACTGCTT GTGCCCTTGC 960
 15 CTGAAAAACT ATGACTTTGG GAGTAGCACT GAGACATCAG ATAGTCACCT CACTAAGGCT 1020
 CTCTCCACCT TCATTCATGC AGAAGATTTT GCCAGGAGGA GGAAGAGGTC TGTGTCACTC 1080
 TAA 1083

(29) INFORMATION FOR SEQ ID NO:28:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 360 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Asp Pro Glu Glu Thr Ser Val Tyr Leu Asp Tyr Tyr Tyr Ala Thr
1 5 10 15

Ser Pro Asn Ser Asp Ile Arg Glu Thr His Ser His Val Pro Tyr Thr
20 25 30

30 Ser Val Phe Leu Pro Val Phe Tyr Thr Ala Val Phe Leu Thr Gly Val
35 40 45

24

Leu Gly Asn Leu Val Leu Met Gly Ala Leu His Phe Lys Pro Gly Ser
 50 55 60

Arg Arg Leu Ile Asp Ile Phe Ile Ile Asn Leu Ala Ala Ser Asp Phe
 65 70 75 80

5 Ile Phe Leu Val Thr Leu Pro Leu Trp Val Asp Lys Glu Ala Ser Leu
 85 90 95

Gly Leu Trp Arg Thr Gly Ser Phe Leu Cys Lys Gly Ser Ser Tyr Met
 100 105 110

10 Ile Ser Val Asn Met His Cys Ser Val Leu Leu Leu Thr Cys Met Ser
 115 120 125

Val Asp Arg Tyr Leu Ala Ile Val Trp Pro Val Val Ser Arg Lys Phe
 130 135 140

Arg Arg Thr Asp Cys Ala Tyr Val Val Cys Ala Ser Ile Trp Phe Ile
 145 150 155 160

15 Ser Cys Leu Leu Gly Leu Pro Thr Leu Leu Ser Arg Glu Leu Thr Leu
 165 170 175

Ile Asp Asp Lys Pro Tyr Cys Ala Glu Lys Lys Ala Thr Pro Ile Lys
 180 185 190

20 Leu Ile Trp Ser Leu Val Ala Leu Ile Phe Thr Phe Phe Val Pro Leu
 195 200 205

Leu Ser Ile Val Thr Cys Tyr Cys Cys Ile Ala Arg Lys Leu Cys Ala
 210 215 220

His Tyr Gln Gln Ser Gly Lys His Asn Lys Lys Leu Lys Lys Ser Ile
 225 230 235 240

25 Lys Ile Ile Phe Ile Val Val Ala Ala Phe Leu Val Ser Trp Leu Pro
 245 250 255

Phe Asn Thr Phe Lys Phe Leu Ala Ile Val Ser Gly Leu Arg Gln Glu
 260 265 270

30 His Tyr Leu Pro Ser Ala Ile Leu Gln Leu Gly Met Glu Val Ser Gly
 275 280 285

Pro Leu Ala Phe Ala Asn Ser Cys Val Asn Pro Phe Ile Tyr Tyr Ile
 290 295 300

Phe Asp Ser Tyr Ile Arg Arg Ala Ile Val His Cys Leu Cys Pro Cys
 305 310 315 320

35 Leu Lys Asn Tyr Asp Phe Gly Ser Ser Thr Glu Thr Ser Asp Ser His
 325 330 335

Leu Thr Lys Ala Leu Ser Thr Phe Ile His Ala Glu Asp Phe Ala Arg

25

340

345

350

Arg Arg Lys Arg Ser Val Ser Leu
355 360

(30) INFORMATION FOR SEQ ID NO:29:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 10 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CTAGAATTCT GACTCCAGCC AAAGCATGAA T

31

(31) INFORMATION FOR SEQ ID NO:30:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GCTGGATCCT AACAGTCTG CGCTCGGCCT

30

(32) INFORMATION FOR SEQ ID NO:31:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1020 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

30 ATGAATGCC TTGAAGTGGC TCCCCAGGT CTGATCACCA ACTTCTCCCT GGCCACGGCA 60
GAGCAATGTG GCCAGGAGAC GCCACTGGAG AACATGCTGT TCGCCTCCTT CTACCTTCTG 120
GATTTTATCC TGGCTTTAGT TGGCAATACC CTGGCTCTGT GGCCTTTTCAT CCGAGACCAC 180
AAGTCCGGGA CCCC GGCCAA CGTGTTCTTG ATGCATCTGG CCGTGGCCGA CTTGTCTGTC 240
GTGCTGGTCC TGCCCACCCG CCTGGTCTAC CACTTCTCTG GGAACCACTG GCCATTTGGG 300

GAAATCGCAT GCCGTCTCAC CGGCTTCCTC TTCTACCTCA ACATGTACGC CAGCATCTAC 360
 TTCCTCACCT GCATCAGCGC CGACCGTTTC CTGGCCATTG TGCACCCGGT CAAGTCCCTC 420
 AAGCTCCGCA GGCCCCCTCTA CGCACACCTG GCCTGTGCCT TCCTGTGGGT GGTGGTGGCT 480
 GTGGCCATGG CCCCCTGCT GGTGAGCCCA CAGACCGTGC AGACCAACCA CACGGTGGTC 540
 5 TGCCTGCAGC TGTACCGGA GAAGGCCTCC CACCATGCCC TGGTGTCCCT GGCAGTGGCC 600
 TTCACCTTCC CGTTCATCAC CACGGTCACC TGCTACCTGC TGATCATCCG CAGCCTGCGG 660
 CAGGGCCTGC GTGTGGAGAA GCGCCTCAAG ACCAAGGCAG TCGCATGAT CGCCATAGTG 720
 CTGGCCATCT TCCTGGTCTG CTTCGTGCCC TACCACGTCA ACCGCTCCGT CTACGTGCTG 780
 CACTACCGCA GCCATGGGGC CTCCTGCGCC ACCCAGCGCA TCCTGGCCCT GGCAAACCGC 840
 10 ATCACCTCCT GCCTCACCAG CCTCAACGGG GCACTCGACC CCATCATGTA TTTCTTCGTG 900
 GCTGAGAAGT TCCGCCACGC CCTGTGCAAC TTGCTCTGTG GCAAAGGCT CAAGGGCCCCG 960
 CCCCCAGCT TCGAAGGGAA AACCAACGAG AGCTCGCTGA GTGCCAAGTC AGAGCTGTGA 1020

(33) INFORMATION FOR SEQ ID NO:32:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 339 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

 (ii) MOLECULE TYPE: protein

 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

 Met Asn Gly Leu Glu Val Ala Pro Pro Gly Leu Ile Thr Asn Phe Ser
 1 5 10 15
 Leu Ala Thr Ala Glu Gln Cys Gly Gln Glu Thr Pro Leu Glu Asn Met
 20 25 30
 25 Leu Phe Ala Ser Phe Tyr Leu Leu Asp Phe Ile Leu Ala Leu Val Gly
 35 40 45
 Asn Thr Leu Ala Leu Trp Leu Phe Ile Arg Asp His Lys Ser Gly Thr
 50 55 60
 30 Pro Ala Asn Val Phe Leu Met His Leu Ala Val Ala Asp Leu Ser Cys
 65 70 75 80
 Val Leu Val Leu Pro Thr Arg Leu Val Tyr His Phe Ser Gly Asn His
 85 90 95
 Trp Pro Phe Gly Glu Ile Ala Cys Arg Leu Thr Gly Phe Leu Phe Tyr

27

	100	105	110
	Leu Asn Met Tyr Ala Ser Ile Tyr Phe Leu Thr Cys Ile Ser Ala Asp		
	115	120	125
5	Arg Phe Leu Ala Ile Val His Pro Val Lys Ser Leu Lys Leu Arg Arg		
	130	135	140
	Pro Leu Tyr Ala His Leu Ala Cys Ala Phe Leu Trp Val Val Val Ala		
	145	150	155 160
	Val Ala Met Ala Pro Leu Leu Val Ser Pro Gln Thr Val Gln Thr Asn		
		165 170	175
10	His Thr Val Val Cys Leu Gln Leu Tyr Arg Glu Lys Ala Ser His His		
		180 185	190
	Ala Leu Val Ser Leu Ala Val Ala Phe Thr Phe Pro Phe Ile Thr Thr		
		195 200	205
15	Val Thr Cys Tyr Leu Leu Ile Ile Arg Ser Leu Arg Gln Gly Leu Arg		
		210 215	220
	Val Glu Lys Arg Leu Lys Thr Lys Ala Val Arg Met Ile Ala Ile Val		
		225 230	235 240
	Leu Ala Ile Phe Leu Val Cys Phe Val Pro Tyr His Val Asn Arg Ser		
		245 250	255
20	Val Tyr Val Leu His Tyr Arg Ser His Gly Ala Ser Cys Ala Thr Gln		
		260 265	270
	Arg Ile Leu Ala Leu Ala Asn Arg Ile Thr Ser Cys Leu Thr Ser Leu		
		275 280	285
25	Asn Gly Ala Leu Asp Pro Ile Met Tyr Phe Phe Val Ala Glu Lys Phe		
		290 295	300
	Arg His Ala Leu Cys Asn Leu Leu Cys Gly Lys Arg Leu Lys Gly Pro		
		305 310	315 320
	Pro Pro Ser Phe Glu Gly Lys Thr Asn Glu Ser Ser Leu Ser Ala Lys		
		325 330	335
30	Ser Glu Leu		

(34) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ATAAGATGAT CACCCTGAAC AATCAAGAT

29

(35) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

TCCGAATTCA TAACATTTC A CTGTTTATAT TGC

33

(36) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 996 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

20 ATGATCACCC TGAACAATCA AGATCAACCT GTCACCTTTTA ACAGCTCACA TCCAGATGAA 60
TACAAAATTG CAGCCCTTGT CTTCTATAGC TGTATCTTCA TAATTGGATT ATTGTGTAAC 120
ATCACTGCAT TATGGGTTTT CAGTTGTACC ACCAAGAAGA GAACCAAGGT AACCATCTAT 180
ATGATGAATG TGGCATTAGT GGACTTGATA TTTATAATGA CTTTACCCTT TCGAATGTTT 240
TATTATGCAA AAGATGCATG GCCATTTGGA GAGTACTTCT GCCAGATTAT TGGAGCTCTC 300
25 ACAGTGTTTT ACCCAAGCAT TGCTTTATGG CTTCTTGCCT TTATTAGTGC TGACAGATAC 360
ATGGCCATTG TACAGCCGAA GTACGCCAAA GAACCTAAAA ACACGTGCAA AGCCGTGCTG 420
GCGTGTGTGG GAGTCTGGAT AATGACCCTG ACCACGACCA CCCCTCTGCT ACTGCTCTAT 480
AAAGACCCAG ATAAAGACTC CACTCCCGCC ACCTGCCTCA AGATTCTCTGA CATCATCTAT 540
CTAAAAGCTG TGAACGTGCT GAACCTCACT CGACTGACAT TTTTTTCTT GATTCCCTTG 600
30 TTCATCATGA TTGGGTGCTA CTTGGTCATT ATTCATAATC TCCTTCACGG CAGGACGTCT 660
AAGCTGAAAC CCAAAGTCAA GGAGAAGTCC ATAAGGATCA TCATCACGCT GCTGGTGCAG 720

GTGCTCGTCT GCTTTATGCC CTTCACATC TGTTTCGCTT TCCTGATGCT GGGAACGGGG 780
 GAGAACAGTT ACAATCCCTG GGGAGCCTTT ACCACCTTCC TCATGAACCT CAGCACGTGT 840
 CTGGATGTGA TTCTCTACTA CATCGTTTCA AAACAATTTT AGGCTCGAGT CATTAGTGTC 900
 ATGCTATACC GTAATTACCT TCGAAGCCTG CGCAGAAAAA GTTCCGATC TGGTAGTCTA 960
 5 AGGTCATAA GCAATATAAA CAGTGAAATG TTATGA 996

(37) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 331 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

15 Met Ile Thr Leu Asn Asn Gln Asp Gln Pro Val Thr Phe Asn Ser Ser
 1 5 10 15
 His Pro Asp Glu Tyr Lys Ile Ala Ala Leu Val Phe Tyr Ser Cys Ile
 20 25 30
 Phe Ile Ile Gly Leu Phe Val Asn Ile Thr Ala Leu Trp Val Phe Ser
 35 40 45
 20 Cys Thr Thr Lys Lys Arg Thr Thr Val Thr Ile Tyr Met Met Asn Val
 50 55 60
 Ala Leu Val Asp Leu Ile Phe Ile Met Thr Leu Pro Phe Arg Met Phe
 65 70 75 80
 25 Tyr Tyr Ala Lys Asp Ala Trp Pro Phe Gly Glu Tyr Phe Cys Gln Ile
 85 90 95
 Ile Gly Ala Leu Thr Val Phe Tyr Pro Ser Ile Ala Leu Trp Leu Leu
 100 105 110
 Ala Phe Ile Ser Ala Asp Arg Tyr Met Ala Ile Val Gln Pro Lys Tyr
 115 120 125
 30 Ala Lys Glu Leu Lys Asn Thr Cys Lys Ala Val Leu Ala Cys Val Gly
 130 135 140
 Val Trp Ile Met Thr Leu Thr Thr Thr Thr Pro Leu Leu Leu Tyr
 145 150 155 160
 35 Lys Asp Pro Asp Lys Asp Ser Thr Pro Ala Thr Cys Leu Lys Ile Ser
 165 170 175

30

Asp Ile Ile Tyr Leu Lys Ala Val Asn Val Leu Asn Leu Thr Arg Leu
 180 185 190
 Thr Phe Phe Phe Leu Ile Pro Leu Phe Ile Met Ile Gly Cys Tyr Leu
 195 200 205
 5 Val Ile Ile His Asn Leu Leu His Gly Arg Thr Ser Lys Leu Lys Pro
 210 215 220
 Lys Val Lys Glu Lys Ser Ile Arg Ile Ile Ile Thr Leu Leu Val Gln
 225 230 235 240
 10 Val Leu Val Cys Phe Met Pro Phe His Ile Cys Phe Ala Phe Leu Met
 245 250 255
 Leu Gly Thr Gly Glu Asn Ser Tyr Asn Pro Trp Gly Ala Phe Thr Thr
 260 265 270
 Phe Leu Met Asn Leu Ser Thr Cys Leu Asp Val Ile Leu Tyr Tyr Ile
 275 280 285
 15 Val Ser Lys Gln Phe Gln Ala Arg Val Ile Ser Val Met Leu Tyr Arg
 290 295 300
 Asn Tyr Leu Arg Ser Leu Arg Arg Lys Ser Phe Arg Ser Gly Ser Leu
 305 310 315 320
 20 Arg Ser Leu Ser Asn Ile Asn Ser Glu Met Leu
 325 330

(38) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CCAAGCTTCC AGGCCTGGGG TGTGCTGG

28

30 (39) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ATGGATCCTG ACCTTCGGCC CCTGGCAGA

29

(40) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 1077 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

10 ATGCCCTCTG TGTCTCCAGC GGGGCCCTCG GCCGGGGCAG TCCCAATGC CACCGCAGTG 60
ACAACAGTGC GGACCAATGC CAGCGGGCTG GAGGTGCCCC TGTTCACCT GTTGCCCCGG 120
CTGGACGAGG AGCTGCATGG CACCTTCCCA GGCCTGTGCG TGGCGCTGAT GGCGGTGCAC 180
GGAGCCATCT TCCTGGCAGG GCTGGTGCTC AACGGGCTGG CGCTGTACGT CTTCTGCTGC 240
CGCACCCGGG CCAAGACACC CTCAGTCATC TACACCATCA ACCTGGTGGT GACCGATCTA 300
15 CTGGTAGGGC TGTCCCTGCC CACGCGCTTC GCTGTGTACT ACGGCGCCAG GGGCTGCCTG 360
CGCTGTGCCT TCCCGCACGT CCTCGGTTAC TTCCTCAACA TGCACTGCTC CATCCTCTTC 420
CTCACCTGCA TCTGCGTGGA CCGCTACCTG GCCATCGTGC GGCCCGAAGG CTCCCGCCGC 480
TGCCGCCAGC CTGCCTGTGC CAGGGCCGTG TGCGCCTTCG TGTGGCTGGC CGCCGGTGCC 540
GTCACCTGT CGGTGCTGGG CGTGACAGG AGCCGGCCCT GCTGCCGTGT CTTTGCCTG 600
20 ACTGTCCTGG AGTTCCTGCT GCCCCTGCTG GTCATCAGCG TGTTTACCG CCGCATCATG 660
TGTGCACTGT CGCGGCCGGG TCTGCTCCAC CAGGGTCGCC AGCGCCGCGT GCGGGCCATG 720
CAGCTCCTGC TCACGGTGCT CATCATCTTT CTCGTCTGCT TCACGCCCTT CCACGCCCGC 780
CAAGTGGCCG TGGCGCTGTG GCCCGACATG CCACACCACA CGAGCCTCGT GGTCTACCAC 840
GTGGCCGTGA CCCTCAGCAG CCTCAACAGC TGCATGGACC CCATCGTCTA CTGCTTCGTC 900
25 ACCAGTGGCT TCCAGGCCAC CGTCCGAGGC CTCTTCGGCC AGCACGGAGA GCGTGAGCCC 960
AGCAGCGGTG ACGTGGTCAG CATGCACAGG AGCTCCAAGG GCTCAGGCCG TCATCACATC 1020
CTCAGTGCCG GCCCTCACGC CCTACCCAG GCCCTGGCTA ATGGGCCCCA GGCTTAG 1077

(41) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 358 amino acids

- (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

```

Met Pro Ser Val Ser Pro Ala Gly Pro Ser Ala Gly Ala Val Pro Asn
1           5           10           15

Ala Thr Ala Val Thr Thr Val Arg Thr Asn Ala Ser Gly Leu Glu Val
           20           25           30

10 Pro Leu Phe His Leu Phe Ala Arg Leu Asp Glu Glu Leu His Gly Thr
           35           40           45

Phe Pro Gly Leu Cys Val Ala Leu Met Ala Val His Gly Ala Ile Phe
           50           55           60

15 Leu Ala Gly Leu Val Leu Asn Gly Leu Ala Leu Tyr Val Phe Cys Cys
           65           70           75           80

Arg Thr Arg Ala Lys Thr Pro Ser Val Ile Tyr Thr Ile Asn Leu Val
           85           90           95

Val Thr Asp Leu Leu Val Gly Leu Ser Leu Pro Thr Arg Phe Ala Val
           100          105          110

20 Tyr Tyr Gly Ala Arg Gly Cys Leu Arg Cys Ala Phe Pro His Val Leu
           115          120          125

Gly Tyr Phe Leu Asn Met His Cys Ser Ile Leu Phe Leu Thr Cys Ile
           130          135          140

25 Cys Val Asp Arg Tyr Leu Ala Ile Val Arg Pro Glu Ala Pro Ala Ala
           145          150          155          160

Cys Arg Gln Pro Ala Cys Ala Arg Ala Val Cys Ala Phe Val Trp Leu
           165          170          175

Ala Ala Gly Ala Val Thr Leu Ser Val Leu Gly Val Thr Gly Ser Arg
           180          185          190

30 Pro Cys Cys Arg Val Phe Ala Leu Thr Val Leu Glu Phe Leu Leu Pro
           195          200          205

Leu Leu Val Ile Ser Val Phe Thr Gly Arg Ile Met Cys Ala Leu Ser
           210          215          220

35 Arg Pro Gly Leu Leu His Gln Gly Arg Gln Arg Val Arg Ala Met
           225          230          235          240

Gln Leu Leu Leu Thr Val Leu Ile Ile Phe Leu Val Cys Phe Thr Pro
           245          250          255

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33

Phe His Ala Arg Gln Val Ala Val Ala Leu Trp Pro Asp Met Pro His
 260 265 270
 His Thr Ser Leu Val Val Tyr His Val Ala Val Thr Leu Ser Ser Leu
 275 280 285
 5 Asn Ser Cys Met Asp Pro Ile Val Tyr Cys Phe Val Thr Ser Gly Phe
 290 295 300
 Gln Ala Thr Val Arg Gly Leu Phe Gly Gln His Gly Glu Arg Glu Pro
 305 310 315 320
 10 Ser Ser Gly Asp Val Val Ser Met His Arg Ser Ser Lys Gly Ser Gly
 325 330 335
 Arg His His Ile Leu Ser Ala Gly Pro His Ala Leu Thr Gln Ala Leu
 340 345 350
 Ala Asn Gly Pro Glu Ala
 355

15 (42) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 20 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GAGAATTCAC TCCTGAGCTC AAGATGAACT

30

(43) INFORMATION FOR SEQ ID NO:42:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CGGGATCCCC GTAAC TGAGC CACTTCAGAT

30

(44) INFORMATION FOR SEQ ID NO:43:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1050 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ATGAACTCCA CCTTGGATGG TAATCAGAGC AGCCACCCTT TTTGCCTCTT GGCATTGCGC 60
 5 TATTTGGAAA CTGTCAATTT TTGCCTTTTG GAAGTATTGA TTATTGTCTT TCTAACTGTA 120
 TTGATTATTT CTGGCAACAT CATTGTGATT TTTGTATTTT ACTGTGCACC TTTGTTGAAC 180
 CATCACACTA CAAGTTATTT TATCCAGACT ATGGCATATG CTGACCTTTT TGTGTTGGGTG 240
 AGCTGCGTGG TCCCTTCTTT ATCACTCCTC CATCACCCCC TTCCAGTAGA GGAGTCCTTG 300
 ACTTGCCAGA TATTTGGTTT TGTAGTATCA GTTCTGAAGA GCGTCTCCAT GGCTTCTCTG 360
 10 GCCTGTATCA GCATTGATAG ATACATTGCC ATTACTAAAC CTTTAACTTA TAATACTCTG 420
 GTTACACCCT GGAGACTACG CCTGTGTATT TTCCTGATTT GGCTATACTC GACCCTGGTC 480
 TTCCTGCCTT CCTTTTTCCTA CTGGGGCAAA CTGGGATATC ATGGAGATGT GTTTCAGTGG 540
 TGTGCGGAGT CCTGGCACAC CGACTCCTAC TTCACCCTGT TCATCGTGAT GATGTTATAT 600
 GCCCCAGCAG CCCTTATTGT CTGCTTCACC TATTTCACCA TCTTCCGCAT CTGCCAACAG 660
 15 CACACAAAGG ATATCAGCGA AAGGCAAGCC CGCTTCAGCA GCCAGAGTGG GGAGACTGGG 720
 GAAGTGCAGG CCTGTCCTGA TAAGCGCTAT GCCATGGTCC TGTTTCGAAT CACTAGTGTA 780
 TTTTACATCC TCTGGTTGCC ATATATCATC TACTTCTTGT TGGAAAGCTC CACTGGCCAC 840
 AGCAACCGCT TCGCATCCTT CTTGACCACC TGGCTTGCTA TTAGTAACAG TTTCTGCAAC 900
 TGTGTAATTT ATAGTCTCTC CAACAGTGTA TTCCAAAGAG GACTAAAGCG CCTCTCAGGG 960
 20 GCTATGTGTA CTTCTTGTGC AAGTCAGACT ACAGCCAACG ACCCTTACAC AGTTAGAAGC 1020
 AAAGGCCCTC TTAATGGATG TCATATCTGA 1050

(45) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

30 Met Asn Ser Thr Leu Asp Gly Asn Gln Ser Ser His Pro Phe Cys Leu

35

	1		5		10		15									
	Leu	Ala	Phe	Gly	Tyr	Leu	Glu	Thr	Val	Asn	Phe	Cys	Leu	Leu	Glu	Val
				20					25						30	
5	Leu	Ile	Ile	Val	Phe	Leu	Thr	Val	Leu	Ile	Ile	Ser	Gly	Asn	Ile	Ile
			35					40					45			
	Val	Ile	Phe	Val	Phe	His	Cys	Ala	Pro	Leu	Leu	Asn	His	His	Thr	Thr
			50				55					60				
	Ser	Tyr	Phe	Ile	Gln	Thr	Met	Ala	Tyr	Ala	Asp	Leu	Phe	Val	Gly	Val
	65					70					75				80	
10	Ser	Cys	Val	Val	Pro	Ser	Leu	Ser	Leu	Leu	His	His	Pro	Leu	Pro	Val
					85					90					95	
	Glu	Glu	Ser	Leu	Thr	Cys	Gln	Ile	Phe	Gly	Phe	Val	Val	Ser	Val	Leu
				100					105					110		
15	Lys	Ser	Val	Ser	Met	Ala	Ser	Leu	Ala	Cys	Ile	Ser	Ile	Asp	Arg	Tyr
			115					120					125			
	Ile	Ala	Ile	Thr	Lys	Pro	Leu	Thr	Tyr	Asn	Thr	Leu	Val	Thr	Pro	Trp
			130				135						140			
	Arg	Leu	Arg	Leu	Cys	Ile	Phe	Leu	Ile	Trp	Leu	Tyr	Ser	Thr	Leu	Val
	145				150						155					160
20	Phe	Leu	Pro	Ser	Phe	Phe	His	Trp	Gly	Lys	Pro	Gly	Tyr	His	Gly	Asp
					165					170					175	
	Val	Phe	Gln	Trp	Cys	Ala	Glu	Ser	Trp	His	Thr	Asp	Ser	Tyr	Phe	Thr
				180					185					190		
25	Leu	Phe	Ile	Val	Met	Met	Leu	Tyr	Ala	Pro	Ala	Ala	Leu	Ile	Val	Cys
			195					200					205			
	Phe	Thr	Tyr	Phe	Asn	Ile	Phe	Arg	Ile	Cys	Gln	Gln	His	Thr	Lys	Asp
	210					215						220				
	Ile	Ser	Glu	Arg	Gln	Ala	Arg	Phe	Ser	Ser	Gln	Ser	Gly	Glu	Thr	Gly
	225				230						235					240
30	Glu	Val	Gln	Ala	Cys	Pro	Asp	Lys	Arg	Tyr	Ala	Met	Val	Leu	Phe	Arg
					245					250					255	
	Ile	Thr	Ser	Val	Phe	Tyr	Ile	Leu	Trp	Leu	Pro	Tyr	Ile	Ile	Tyr	Phe
				260					265					270		
35	Leu	Leu	Glu	Ser	Ser	Thr	Gly	His	Ser	Asn	Arg	Phe	Ala	Ser	Phe	Leu
			275					280					285			
	Thr	Thr	Trp	Leu	Ala	Ile	Ser	Asn	Ser	Phe	Cys	Asn	Cys	Val	Ile	Tyr
			290				295						300			

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Ser Leu Ser Asn Ser Val Phe Gln Arg Gly Leu Lys Arg Leu Ser Gly
 305 310 315 320
 Ala Met Cys Thr Ser Cys Ala Ser Gln Thr Thr Ala Asn Asp Pro Tyr
 325 330 335
 5 Thr Val Arg Ser Lys Gly Pro Leu Asn Gly Cys His Ile
 340 345

(46) INFORMATION FOR SEQ ID NO:45:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

15 TCCCCCGGGA AAAAAACCAA CTGCTCCAAA 30

(47) INFORMATION FOR SEQ ID NO:46:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TAGGATCCAT TTGAATGTGG ATTTGGTGAA A 31

25 (48) INFORMATION FOR SEQ ID NO:47:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1302 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ATGTGTTTTT CTCCATTCT GGAAATCAAC ATGCGAGTCTG AATCTAACAT TACAGTGCGA 60
 GATGACATTG ATGACATCAA CACCAATATG TACCAACCAC TATCATATCC GTTAAGCTTT 120
 35 CAAGTGTCTC TCACCGGATT TCTTATGTGA GAAATTGTGT TGGGACTTGG CAGCAACCTC 180

ACTGTATTGG TACTTTACTG CATGAAATCC AACTTAATCA ACTCTGTCAG TAACATTATT 240
 ACAATGAATC TTCATGTACT TGATGTAATA ATTTGTGTGG GATGTATTCC TCTAACTATA 300
 GTTATCCTTC TGCTTTCACT GGAGAGTAAC ACTGCTCTCA TTTGCTGTTT CCATGAGGCT 360
 TGTGTATCTT TTGCAAGTGT CTCAACAGCA ATCAACGTTT TTGCTATCAC TTTGGACAGA 420
 5 TATGACATCT CTGTAAAACC TGCAAACCGA ATTCTGACAA TGGGCAGAGC TGTAATGTTA 480
 ATGATATCCA TTTGGATTTT TTCTTTTTTC TCTTCTCTGA TTCCTTTTAT TGAGGTAAAT 540
 TTTTTCAGTC TTCAAAGTGG AAATACCTGG GAAAACAAGA CACTTTTATG TGTCAGTACA 600
 AATGAATACT AACTGAACT GGAATGTAT TATCACCTGT TAGTACAGAT CCCAATATTC 660
 TTTTCACTG TTGTAGTAAT GTTAATCACA TACACCAAAA TACTTCAGGC TCTTAATATT 720
 10 CGAATAGGCA CAAGATTTTC AACAGGGCAG AAGAAGAAAG CAAGAAAGAA AAAGACAATT 780
 TCTCTAACCA CACAACATGA GGCTACAGAC ATGTCACAAA GCAGTGGTGG GAGAAATGTA 840
 GTCTTTGGTG TAAGAACTTC AGTTTCTGTA ATAATTGCCC TCCGGCGAGC TGTGAAACGA 900
 CACCGTGAAC GACGAGAAAG ACAAAGAGA GTCTTCAGGA TGTCTTTATT GATTATTTCT 960
 ACATTTCTTC TCTGCTGGAC ACCAATTTCT GTTTTAAATA CCACCATTTT ATGTTTAGGC 1020
 15 CCAAGTGACC TTTTAGTAAA ATTAAGATTG TGTTTTTTAG TCATGGCTTA TGGAACAACT 1080
 ATATTTTACC CTCTATTATA TGCATTCCT AGACAAAAAT TTCAAAGGT CTTGAAAAGT 1140
 AAAATGAAAA AGCGAGTTGT TTCTATAGTA GAAGCTGATC CCCTGCCTAA TAATGCTGTA 1200
 ATACACAACT CTGGATAGA TCCCAAAAGA AACAAAAAAA TTACCTTTGA AGATAGTGAA 1260
 ATAAGAGAAA AACGTTTAGT GCCTCAGGTT GTCACAGACT AG 1302

20 (49) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 433 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 25 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Met Cys Phe Ser Pro Ile Leu Glu Ile Asn Met Gln Ser Glu Ser Asn
 1 5 10 15

30 Ile Thr Val Arg Asp Asp Ile Asp Asp Ile Asn Thr Asn Met Tyr Gln
 20 25 30

Pro Leu Ser Tyr Pro Leu Ser Phe Gln Val Ser Leu Thr Gly Phe Leu
 35 40 45
 Met Leu Glu Ile Val Leu Gly Leu Gly Ser Asn Leu Thr Val Leu Val
 50 55 60
 5 Leu Tyr Cys Met Lys Ser Asn Leu Ile Asn Ser Val Ser Asn Ile Ile
 65 70 75 80
 Thr Met Asn Leu His Val Leu Asp Val Ile Ile Cys Val Gly Cys Ile
 85 90 95
 10 Pro Leu Thr Ile Val Ile Leu Leu Leu Ser Leu Glu Ser Asn Thr Ala
 100 105 110
 Leu Ile Cys Cys Phe His Glu Ala Cys Val Ser Phe Ala Ser Val Ser
 115 120 125
 Thr Ala Ile Asn Val Phe Ala Ile Thr Leu Asp Arg Tyr Asp Ile Ser
 130 135 140
 15 Val Lys Pro Ala Asn Arg Ile Leu Thr Met Gly Arg Ala Val Met Leu
 145 150 155 160
 Met Ile Ser Ile Trp Ile Phe Ser Phe Phe Ser Phe Leu Ile Pro Phe
 165 170 175
 20 Ile Glu Val Asn Phe Phe Ser Leu Gln Ser Gly Asn Thr Trp Glu Asn
 180 185 190
 Lys Thr Leu Leu Cys Val Ser Thr Asn Glu Tyr Tyr Thr Glu Leu Gly
 195 200 205
 Met Tyr Tyr His Leu Leu Val Gln Ile Pro Ile Phe Phe Phe Thr Val
 210 215 220
 25 Val Val Met Leu Ile Thr Tyr Thr Lys Ile Leu Gln Ala Leu Asn Ile
 225 230 235 240
 Arg Ile Gly Thr Arg Phe Ser Thr Gly Gln Lys Lys Lys Ala Arg Lys
 245 250 255
 30 Lys Lys Thr Ile Ser Leu Thr Thr Gln His Glu Ala Thr Asp Met Ser
 260 265 270
 Gln Ser Ser Gly Gly Arg Asn Val Val Phe Gly Val Arg Thr Ser Val
 275 280 285
 Ser Val Ile Ile Ala Leu Arg Arg Ala Val Lys Arg His Arg Glu Arg
 290 295 300
 35 Arg Glu Arg Gln Lys Arg Val Phe Arg Met Ser Leu Leu Ile Ile Ser
 305 310 315 320
 Thr Phe Leu Leu Cys Trp Thr Pro Ile Ser Val Leu Asn Thr Thr Ile

39

					325					330					335	
	Leu	Cys	Leu	Gly	Pro	Ser	Asp	Leu	Leu	Val	Lys	Leu	Arg	Leu	Cys	Phe
				340						345					350	
5	Leu	Val	Met	Ala	Tyr	Gly	Thr	Thr	Ile	Phe	His	Pro	Leu	Leu	Tyr	Ala
			355					360						365		
	Phe	Thr	Arg	Gln	Lys	Phe	Gln	Lys	Val	Leu	Lys	Ser	Lys	Met	Lys	Lys
		370					375					380				
	Arg	Val	Val	Ser	Ile	Val	Glu	Ala	Asp	Pro	Leu	Pro	Asn	Asn	Ala	Val
	385					390					395					400
10	Ile	His	Asn	Ser	Trp	Ile	Asp	Pro	Lys	Arg	Asn	Lys	Lys	Ile	Thr	Phe
					405						410				415	
	Glu	Asp	Ser	Glu	Ile	Arg	Glu	Lys	Arg	Leu	Val	Pro	Gln	Val	Val	Thr
				420					425					430		

Asp

15

(50) INFORMATION FOR SEQ ID NO:49:

(i). SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GTGAAGCTTG CCTCTGGTGC CTGCAGGAGG

30

25 (51) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GCAGAATTCC CGGTGGCGTG TTGTGGTGCC C

31

(52) INFORMATION FOR SEQ ID NO:51:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1209 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

	ATGTTGTGTC CTTCCAAGAC AGATGGCTCA GGGCACTCTG GTAGGATTCA CCAGGAAACT	60
	CATGGAGAAG GGAAAAGGGA CAAGATTAGC AACAGTGAAG GGAGGGAGAA TGGTGGGAGA	120
	GGATTCCAGA TGAACGGTGG GTCGCTGGAG GCTGAGCATG CCAGCAGGAT GTCAGTTCTC	180
	AGAGCAAAGC CCATGTCAAA CAGCCAACGC TTGCTCCTTC TGTCCCCAGG ATCACCTCCT	240
10	CGCACGGGGA GCATCTCCTA CATCAACATC ATCATGCCTT CGGTGTTCGG CACCATCTGC	300
	CTCCTGGGCA TCATCGGGAA CTCCACGGTC ATCTTCGCGG TCGTGAAGAA GTCCAAGCTG	360
	CACTGGTGCA ACAACGTCCC CGACATCTTC ATCATCAACC TCTCGGTAGT AGATCTCCTC	420
	TTTCTCCTGG GCATGCCCTT CATGATCCAC CAGCTCATGG GCAATGGGGT GTGGCACTTT	480
	GGGGAGACCA TGTGCACCCT CATCACGGCC ATGGATGCCA ATAGTCAGTT CACCAGCACC	540
15	TACATCCTGA CCGCCATGGC CATTGACCGC TACCTGGCCA CTGTCCACCC CATCTCTTCC	600
	ACGAAGTTCC GGAAGCCCTC TGTGGCCACC CTGGTGATCT GCCTCCTGTG GGCCCTCTCC	660
	TTCATCAGCA TCACCCTGT GTGGCTGTAT GCCAGACTCA TCCCCTTCCC AGGAGGTGCA	720
	GTGGGCTGCG GCATACGCCT GCCCAACCCA GACACTGACC TCTACTGGTT CACCCTGTAC	780
	CAGTTTTTCC TGGCCTTTGC CCTGCCTTTT GTGGTCATCA CAGCCGCATA CGTGAGGATC	840
20	CTGCAGCGCA TGACGTCTC AGTGGCCCCC GCCTCCCAGC GCAGCATCCG GCTGCGGACA	900
	AAGAGGGTGA CCCGCACAGC CATCGCCATC TGTCTGGTCT TCTTTGTGTG CTGGGCACCC	960
	TACTATGTGC TACAGCTGAC CCAGTTGTCC ATCAGCCGCC CGACCCTCAC CTTTGTCTAC	1020
	TTATACAATG CGGCCATCAG CTTGGGCTAT GCCAACAGCT GCCTCAACCC CTTTGTGTAC	1080
	ATCGTGCTCT GTGAGACGTT CCGCAAACGC TTGGTCCTGT CGGTGAAGCC TGCAGCCCAG	1140
25	GGGCAGCTTC GCGCTGTCAG CAACGCTCAG ACGGCTGACG AGGAGAGGAC AGAAAGCAAA	1200
	GGCACCTGA	1209

(53) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 402 amino acids
 (B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

5 Met Leu Cys Pro Ser Lys Thr Asp Gly Ser Gly His Ser Gly Arg Ile
 1 5 10 15
 His Gln Glu Thr His Gly Glu Gly Lys Arg Asp Lys Ile Ser Asn Ser
 20 25 30
 Glu Gly Arg Glu Asn Gly Gly Arg Gly Phe Gln Met Asn Gly Gly Ser
 10 35 40 45
 Leu Glu Ala Glu His Ala Ser Arg Met Ser Val Leu Arg Ala Lys Pro
 50 55 60
 Met Ser Asn Ser Gln Arg Leu Leu Leu Leu Ser Pro Gly Ser Pro Pro
 65 70 75 80
 15 Arg Thr Gly Ser Ile Ser Tyr Ile Asn Ile Ile Met Pro Ser Val Phe
 85 90 95
 Gly Thr Ile Cys Leu Leu Gly Ile Ile Gly Asn Ser Thr Val Ile Phe
 100 105 110
 Ala Val Val Lys Lys Ser Lys Leu His Trp Cys Asn Asn Val Pro Asp
 115 120 125
 20 Ile Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu Phe Leu Leu Gly
 130 135 140
 Met Pro Phe Met Ile His Gln Leu Met Gly Asn Gly Val Trp His Phe
 145 150 155 160
 25 Gly Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp Ala Asn Ser Gln
 165 170 175
 Phe Thr Ser Thr Tyr Ile Leu Thr Ala Met Ala Ile Asp Arg Tyr Leu
 180 185 190
 Ala Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg Lys Pro Ser Val
 195 200 205
 30 Ala Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser Phe Ile Ser Ile
 210 215 220
 Thr Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe Pro Gly Gly Ala
 225 230 235 240
 35 Val Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr Asp Leu Tyr Trp
 245 250 255

42

[illegible]

(54) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GGCGGATCCA TGGATGTGAC TTCCCAA

27

30 (55) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GGCGGATCCC TACACGGCAC TGCTGAA

27

(56) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1128 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

10 ATGGATGTGA CTTCCCAAGC CCGGGGCGTG GGCCTGGAGA TGTACCCAGG CACCGGCAC 60
GCTGCGGCCC CCAACACCAC CTCCCCGAG CTCAACCTGT CCCACCCGCT CCTGGGCACC 120
GCCCTGGCCA ATGGGACAGG TGAGCTCTCG GAGCACCAGC AGTACGTGAT CGGCCTGTTC 180
CTCTCGTGCC TCTACACCAT CTTCTCTTC CCCATCGGCT TTGTGGGCAA CATCCTGATC 240
CTGGTGGTGA ACATCAGCTT CCGCGAGAAG ATGACCATCC CCGACCTGTA CTTTCATCAAC 300
15 CTGGCGGTGG CGGACCTCAT CCTGGTGGCC GACTCCCTCA TTGAGGTGTT CAACCTGCAC 360
GAGCGGTACT ACGACATCGC CGTCCTGTGC ACCTTCATGT CGCTCTTCCT GCAGGTCAAC 420
ATGTACAGCA GCGTCTTCTT CCTCACCTGG ATGAGCTTCG ACCGCTACAT CGCCCTGGCC 480
AGGGCCATGC GCTGCAGCCT GTTCCGCACC AAGCACCACG CCCGGCTGAG CTGTGGCCTC 540
ATCTGGATGG CATCCGTGTC AGCCACGCTG GTGCCCTTCA CCGCCGTGCA CCTGCAGCAC 600
20 ACCGACGAGG CCTGCTTCTG TTTCGCGGAT GTCCGGGAGG TGCAGTGGCT CGAGGTCACG 660
CTGGGCTTCA TCGTGCCCTT CGCCATCATC GGCCTGTGCT ACTCCCTCAT TGTCCGGGTG 720
CTGGTCAGGG CGCACC GGCA CCGTGGGCTG CGGCCCCGGC GGCAGAAGGC GCTCCGCATG 780
ATCCTCGCGG TGGTGCTGGT CTTCTTCGTC TGCTGGCTGC CGGAGAACGT CTTTCATCAGC 840
GTGCACCTCC TGCAGCGGAC GCAGCCTGGG GCCGCTCCCT GCAAGCAGTC TTTCCGCCAT 900
25 GCCCCACCCC TCACGGGCCA CATTGTCAAC CTCGCCGCCT TCTCCAACAG CTGCCTAAAC 960
CCCCTCATCT ACAGCTTTCT CGGGGAGACC TTCAGGGACA AGCTGAGGCT GTACATTGAG 1020
CAGAAAACAA ATTTGCCGGC CCTGAACCGC TTCTGTCACG CTGCCCTGAA GGCCGTCATT 1080
CCAGACAGCA CCGAGCAGTC GGATGTGAGG TTCAGCAGTG CCGTGTGA 1128

(57) INFORMATION FOR SEQ ID NO:56:

- 30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

5 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

	Met	Asp	Val	Thr	Ser	Gln	Ala	Arg	Gly	Val	Gly	Leu	Glu	Met	Tyr	Pro	
	1				5				10					15			
	Gly	Thr	Ala	His	Ala	Ala	Ala	Pro	Asn	Thr	Thr	Ser	Pro	Glu	Leu	Asn	
10				20				25					30				
	Leu	Ser	His	Pro	Leu	Leu	Gly	Thr	Ala	Leu	Ala	Asn	Gly	Thr	Gly	Glu	
			35				40					45					
	Leu	Ser	Glu	His	Gln	Gln	Tyr	Val	Ile	Gly	Leu	Phe	Leu	Ser	Cys	Leu	
			50				55					60					
15	Tyr	Thr	Ile	Phe	Leu	Phe	Pro	Ile	Gly	Phe	Val	Gly	Asn	Ile	Leu	Ile	
	65				70					75					80		
	Leu	Val	Val	Asn	Ile	Ser	Phe	Arg	Glu	Lys	Met	Thr	Ile	Pro	Asp	Leu	
				85					90					95			
	Tyr	Phe	Ile	Asn	Leu	Ala	Val	Ala	Asp	Leu	Ile	Leu	Val	Ala	Asp	Ser	
20				100					105					110			
	Leu	Ile	Glu	Val	Phe	Asn	Leu	His	Glu	Arg	Tyr	Tyr	Asp	Ile	Ala	Val	
			115				120						125				
	Leu	Cys	Thr	Phe	Met	Ser	Leu	Phe	Leu	Gln	Val	Asn	Met	Tyr	Ser	Ser	
			130				135					140					
25	Val	Phe	Phe	Leu	Thr	Trp	Met	Ser	Phe	Asp	Arg	Tyr	Ile	Ala	Leu	Ala	
	145					150					155				160		
	Arg	Ala	Met	Arg	Cys	Ser	Leu	Phe	Arg	Thr	Lys	His	His	Ala	Arg	Leu	
				165					170						175		
	Ser	Cys	Gly	Leu	Ile	Trp	Met	Ala	Ser	Val	Ser	Ala	Thr	Leu	Val	Pro	
30				180					185					190			
	Phe	Thr	Ala	Val	His	Leu	Gln	His	Thr	Asp	Glu	Ala	Cys	Phe	Cys	Phe	
			195				200						205				
	Ala	Asp	Val	Arg	Glu	Val	Gln	Trp	Leu	Glu	Val	Thr	Leu	Gly	Phe	Ile	
			210				215					220					
35	Val	Pro	Phe	Ala	Ile	Ile	Gly	Leu	Cys	Tyr	Ser	Leu	Ile	Val	Arg	Val	
	225				230					235					240		
	Leu	Val	Arg	Ala	His	Arg	His	Arg	Gly	Leu	Arg	Pro	Arg	Arg	Gln	Lys	

245

255

5

Thr Gly His Ile Val Asn Leu Ala Ala Phe Ser Asn Ser Cys Leu Asn
305 310 315 320

10

Leu Tyr Ile Glu Gln Lys Thr Asn Leu Pro Ala Leu Asn Arg Phe Cys
340 345 350

15

His Ala Ala Leu Lys Ala Val Ile Pro Asp Ser Thr Glu Gln Ser Asp
355 360 365

Val Arg Phe Ser Ser Ala Val
370 375

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

AAGGAATTCA CGGCCGGGTG ATGCCATTCC C

31

(59) INFORMATION FOR SEQ ID NO:58:

30

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

35

GGTGGATCCA TAAACACGGG CGTTGAGGAC

30

(60) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 960 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

ATGCCATTCC CAAACTGCTC AGCCCCCAGC ACTGTGGTGG CCACAGCTGT GGGTGTCTTG 60
 CTGGGGCTGG AGTGTGGGCT GGGTCTGCTG GGCAACGCGG TGGCGCTGTG GACCTTCCTG 120
 10 TTCCGGGTCA GGGTGTGGAA GCCGTACGCT GTCTACCTGC TCAACCTGGC CCTGGCTGAC 180
 CTGCTGTTGG CTGCGTGCCT GCCTTTCCTG GCCGCTTCT ACCTGAGCCT CCAGGCTTGG 240
 CATCTGGGCC GTGTGGGCTG CTGGGCCCTG CGCTTCCTGC TGGACCTCAG CCGCAGCGTG 300
 GGGATGGCCT TCCTGGCCGC CGTGGCTTTG GACCGGTACC TCCGTGTGGT CCACCCTCGG 360
 CTTAAGGTCA ACCTGCTGTC TCCTCAGGCG GCCCTGGGGG TCTCGGGCCT CGTCTGGCTC 420
 15 CTGATGGTCG CCCTCACCTG CCCGGGCTTG CTCATCTCTG AGGCCGCCCA GAACTCCACC 480
 AGGTGCCACA GTTTCTACTC CAGGGCAGAC GGCTCCTTCA GCATCATCTG GCAGGAAGCA 540
 CTCTCCTGCC TTCAGTTTGT CCTCCCCTTT GGCCTCATCG TGTTCTGCAA TGCAGGCATC 600
 ATCAGGGCTC TCCAGAAAAG ACTCCGGGAG CCTGAGAAAC AGCCCAAGCT TCAGCGGGCC 660
 CAGGCACTGG TCACCTTGGT GGTGGTGTCTG TTTGCTCTGT GCTTTCTGCC CTGCTTCCTG 720
 20 GCCAGAGTCC TGATGCACAT CTTCCAGAAT CTGGGGAGCT GCAGGGCCCT TTTGTGCACTG 780
 GCTCATACCT CGGATGTCAC GGGCAGCCTC ACCTACCTGC ACAGTGTCGT CAACCCCGTG 840
 GTATACTGCT TCTCCAGCCC CACCTTCAGG AGCTCCTATC GGAGGGTCTT CCACACCCTC 900
 CGAGGCAAAG GGCAGGCAGC AGAGCCCCCA GATTTCAACC CCAGAGACTC CTATTCTGA 960

(61) INFORMATION FOR SEQ ID NO:60:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 319 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Met Pro Phe Pro Asn Cys Ser Ala Pro Ser Thr Val Val Ala Thr Ala

47

	1		5		10		15									
	Val	Gly	Val	Leu	Leu	Gly	Leu	Glu	Cys	Gly	Leu	Gly	Leu	Leu	Gly	Asn
				20				25						30		
5	Ala	Val	Ala	Leu	Trp	Thr	Phe	Leu	Phe	Arg	Val	Arg	Val	Trp	Lys	Pro
			35					40					45			
	Tyr	Ala	Val	Tyr	Leu	Leu	Asn	Leu	Ala	Leu	Ala	Asp	Leu	Leu	Leu	Ala
		50					55					60				
	Ala	Cys	Leu	Pro	Phe	Leu	Ala	Ala	Phe	Tyr	Leu	Ser	Leu	Gln	Ala	Trp
	65				70					75						80
10	His	Leu	Gly	Arg	Val	Gly	Cys	Trp	Ala	Leu	Arg	Phe	Leu	Leu	Asp	Leu
					85					90					95	
	Ser	Arg	Ser	Val	Gly	Met	Ala	Phe	Leu	Ala	Ala	Val	Ala	Leu	Asp	Arg
				100					105					110		
	Tyr	Leu	Arg	Val	Val	His	Pro	Arg	Leu	Lys	Val	Asn	Leu	Leu	Ser	Pro
15			115					120					125			
	Gln	Ala	Ala	Leu	Gly	Val	Ser	Gly	Leu	Val	Trp	Leu	Leu	Met	Val	Ala
		130					135					140				
	Leu	Thr	Cys	Pro	Gly	Leu	Leu	Ile	Ser	Glu	Ala	Ala	Gln	Asn	Ser	Thr
	145					150				155						160
20	Arg	Cys	His	Ser	Phe	Tyr	Ser	Arg	Ala	Asp	Gly	Ser	Phe	Ser	Ile	Ile
					165					170					175	
	Trp	Gln	Glu	Ala	Leu	Ser	Cys	Leu	Gln	Phe	Val	Leu	Pro	Phe	Gly	Leu
				180					185					190		
	Ile	Val	Phe	Cys	Asn	Ala	Gly	Ile	Ile	Arg	Ala	Leu	Gln	Lys	Arg	Leu
25			195					200					205			
	Arg	Glu	Pro	Glu	Lys	Gln	Pro	Lys	Leu	Gln	Arg	Ala	Gln	Ala	Leu	Val
		210					215					220				
	Thr	Leu	Val	Val	Val	Leu	Phe	Ala	Leu	Cys	Phe	Leu	Pro	Cys	Phe	Leu
	225					230					235					240
30	Ala	Arg	Val	Leu	Met	His	Ile	Phe	Gln	Asn	Leu	Gly	Ser	Cys	Arg	Ala
					245					250					255	
	Leu	Cys	Ala	Val	Ala	His	Thr	Ser	Asp	Val	Thr	Gly	Ser	Leu	Thr	Tyr
			260						265					270		
	Leu	His	Ser	Val	Val	Asn	Pro	Val	Val	Tyr	Cys	Phe	Ser	Ser	Pro	Thr
35			275					280					285			
	Phe	Arg	Ser	Ser	Tyr	Arg	Arg	Val	Phe	His	Thr	Leu	Arg	Gly	Lys	Gly
		290					295						300			

Gln Ala Ala Glu Pro Pro Asp Phe Asn Pro Arg Asp Ser Tyr Ser
 305 310 315

(62) INFORMATION FOR SEQ ID NO:61:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1143 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

ATGGAGGAAG GTGGTGATTT TGACAACTAC TATGGGGCAG ACAACCAGTC TGAGTGTGAG 60
 TACACAGACT GGAAATCCTC GGGGGCCCTC ATCCCTGCCA TCTACATGTT GGTCTTCCTC 120
 CTGGGCACCA CGGGAAACGG TCTGGTGCTC TGGACCGTGT TTCGGAGCAG CCGGGAGAAG 180
 AGGCGCTCAG CTGATATCTT CATTGCTAGC CTGGCGGTGG CTGACCTGAC CTTCGTGGTG 240
 15 ACGCTGCCCC TGTGGGCTAC CTACACGTAC CGGGACTATG ACTGGCCCTT TGGGACCTTC 300
 TTCTGCAAGC TCAGCAGCTA CCTCATCTTC GTCAACATGT ACGCCAGCGT CTTCTGCCTC 360
 ACCGGCCTCA GCTTCGACCG CTACCTGGCC ATCGTGAGGC CAGTGGCCAA TGCTCGGCTG 420
 AGGCTGCGGG TCAGCGGGGC CGTGGCCACG GCAGTTCTTT GGGTGCTGGC CGCCCTCCTG 480
 GCCATGCCTG TCATGGTGTT ACGCACCACC GGGGACTTGG AGAACACCAC TAAGGTGCAG 540
 20 TGCTACATGG ACTACTCCAT GGTGGCCACT GTGAGCTCAG AGTGGGCCTG GGAGGTGGGC 600
 CTTGGGGTCT CGTCCACCAC CGTGGGCTTT GTGGTGCCCT TCACCATCAT GCTGACCTGT 660
 TACTTCTTCA TCGCCCAAAC CATCGCTGGC CACTTCCGCA AGGAACGCAT CGAGGGCCTG 720
 CGGAAGCGGC GCCGGCTGCT CAGCATCATC GTGGTGCTGG TGGTGACCTT TGCCCTGTGC 780
 TGGATGCCCT ACCACCTGGT GAAGACGCTG TACATGCTGG GCAGCCTGCT GCACTGGCCC 840
 25 TGTGACTTTG ACCTCTTCCT CATGAACATC TTCCCCTACT GCACCTGCAT CAGCTACGTC 900
 AACAGCTGCC TCAACCCCTT CCTCTATGCC TTTTTCGACC CCCGCTTCCG CCAGGCCTGC 960
 ACCTCCATGC TCTGCTGTGG CCAGAGCAGG TGCGCAGGCA CCTCCACAG CAGCAGTGGG 1020
 GAGAAGTCAG CCAGCTACTC TTCGGGGCAC AGCCAGGGGC CCGGCCCCAA CATGGGCAAG 1080
 GGTGGAGAAC AGATGCACGA GAAATCCATC CCCTACAGCC AGGAGACCCT TGTGGTTGAC 1140
 30 TAG 1143

(63) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

10 Met Glu Glu Gly Gly Asp Phe Asp Asn Tyr Tyr Gly Ala Asp Asn Gln
 1 5 10 15
 Ser Glu Cys Glu Tyr Thr Asp Trp Lys Ser Ser Gly Ala Leu Ile Pro
 20 25 30
 Ala Ile Tyr Met Leu Val Phe Leu Leu Gly Thr Thr Gly Asn Gly Leu
 35 40 45
 15 Val Leu Trp Thr Val Phe Arg Ser Ser Arg Glu Lys Arg Arg Ser Ala
 50 55 60
 Asp Ile Phe Ile Ala Ser Leu Ala Val Ala Asp Leu Thr Phe Val Val
 65 70 75 80
 20 Thr Leu Pro Leu Trp Ala Thr Tyr Thr Tyr Arg Asp Tyr Asp Trp Pro
 85 90 95
 Phe Gly Thr Phe Phe Cys Lys Leu Ser Ser Tyr Leu Ile Phe Val Asn
 100 105 110
 Met Tyr Ala Ser Val Phe Cys Leu Thr Gly Leu Ser Phe Asp Arg Tyr
 115 120 125
 25 Leu Ala Ile Val Arg Pro Val Ala Asn Ala Arg Leu Arg Leu Arg Val
 130 135 140
 Ser Gly Ala Val Ala Thr Ala Val Leu Trp Val Leu Ala Ala Leu Leu
 145 150 155 160
 30 Ala Met Pro Val Met Val Leu Arg Thr Thr Gly Asp Leu Glu Asn Thr
 165 170 175
 Thr Lys Val Gln Cys Tyr Met Asp Tyr Ser Met Val Ala Thr Val Ser
 180 185 190
 Ser Glu Trp Ala Trp Glu Val Gly Leu Gly Val Ser Ser Thr Thr Val
 195 200 205
 35 Gly Phe Val Val Pro Phe Thr Ile Met Leu Thr Cys Tyr Phe Phe Ile
 210 215 220
 Ala Gln Thr Ile Ala Gly His Phe Arg Lys Glu Arg Ile Glu Gly Leu

	225					230						235					240
	Arg	Lys	Arg	Arg	Arg	Leu	Leu	Ser	Ile	Ile	Val	Val	Leu	Val	Val	Thr	
						245					250					255	
5	Phe	Ala	Leu	Cys	Trp	Met	Pro	Tyr	His	Leu	Val	Lys	Thr	Leu	Tyr	Met	
				260					265						270		
	Leu	Gly	Ser	Leu	Leu	His	Trp	Pro	Cys	Asp	Phe	Asp	Leu	Phe	Leu	Met	
			275					280					285				
	Asn	Ile	Phe	Pro	Tyr	Cys	Thr	Cys	Ile	Ser	Tyr	Val	Asn	Ser	Cys	Leu	
		290					295					300					
10	Asn	Pro	Phe	Leu	Tyr	Ala	Phe	Phe	Asp	Pro	Arg	Phe	Arg	Gln	Ala	Cys	
	305					310					315					320	
	Thr	Ser	Met	Leu	Cys	Cys	Gly	Gln	Ser	Arg	Cys	Ala	Gly	Thr	Ser	His	
					325					330					335		
	Ser	Ser	Ser	Gly	Glu	Lys	Ser	Ala	Ser	Tyr	Ser	Ser	Gly	His	Ser	Gln	
15				340						345				350			
	Gly	Pro	Gly	Pro	Asn	Met	Gly	Lys	Gly	Gly	Glu	Gln	Met	His	Glu	Lys	
			355					360					365				
	Ser	Ile	Pro	Tyr	Ser	Gln	Glu	Thr	Leu	Val	Val	Asp					
		370					375					380					

20 (64) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

TGAGAATTCT GGTGACTCAC AGCCGGCACA G

31

(65) INFORMATION FOR SEQ ID NO:64:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GCCGGATCCA AGGAAAAGCA GCAATAAAAG G

31

(66) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1119 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

10 ATGAACTACC CGTAACGCT GGAAATGGAC CTCGAGAACC TGGAGGACCT GTTCTGGGAA 60
CTGGACAGAT TGGACAACTA TAACGACACC TCCCTGGTGG AAAATCATCT CTGCCCTGCC 120
ACAGAGGGTC CCCTCATGGC CTCCTTCAAG GCCGTGTTCTG TGCCCGTGGC CTACAGCCTC 180
ATCTTCCTCC TGGGCGTGAT CGGCAACGTC CTGGTGCTGG TGATCCTGGA GCGGCACCGG 240
CAGACACGCA GTTCCACGGA GACCTTCTCTG TTCCACCTGG CCGTGGCCGA CCTCCTGCTG 300
15 GTCTTCATCT TGCCCTTTGC CGTGGCCGAG GGCTCTGTGG GCTGGGTCCT GGGGACCTTC 360
CTCTGCAAAA CTGTGATTGC CCTGCACAAA GTCAACTTCT ACTGCAGCAG CCTGCTCCTG 420
GCCTGCATCG CCGTGGACCG CTACCTGGCC ATTGTCCACG CCGTCCATGC CTACCGCCAC 480
CGCCGCCTCC TCTCCATCCA CATCACCTGT GGGACCATCT GGCTGGTGGG CTTCTCCTT 540
GCCTTGCCAG AGATTCTCTT CGCCAAAGTC AGCCAAGGCC ATCACAACAA CTCCCTGCCA 600
20 CGTTGCACCT TCTCCCAAGA GAACCAAGCA GAAACGCATG CCTGGTTCAC CTCCCGATTC 660
CTCTACCATG TGGCGGGATT CCTGCTGCCC ATGCTGGTGA TGGGCTGGTG CTACGTGGGG 720
GTAGTGACA GGTGCGCCA GGCCAGCGG CGCCCTCAGC GGCAGAAGGC AGTCAGGGTG 780
GCCATCCTGG TGACAAGCAT CTTCTTCTC TGCTGGTCAC CCTACCACAT CGTCATCTTC 840
CTGGACACCC TGGCGAGGCT GAAGGCCGTG GACAATACCT GCAAGCTGAA TGGCTCTCTC 900
25 CCCGTGGCCA TCACCATGTG TGAGTTCCTG GGCCTGGCCC ACTGCTGCCT CAACCCCATG 960
CTCTACACTT TCGCCGGCGT GAAGTTCGCG AGTGACCTGT CGCGGCTCCT GACCAAGCTG 1020
GGCTGTACCG GCCCTGCCTC CCTGTGCCAG CTCTTCCCTA GCTGGCGCAG GAGCAGTCTC 1080
TCTGAGTCAG AGAATGCCAC CTCTCTCACC ACGTTCTAG 1119

(67) INFORMATION FOR SEQ ID NO:66:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 372 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: not relevant

5 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

	Met	Asn	Tyr	Pro	Leu	Thr	Leu	Glu	Met	Asp	Leu	Glu	Asn	Leu	Glu	Asp
	1				5						10					15
10	Leu	Phe	Trp	Glu	Leu	Asp	Arg	Leu	Asp	Asn	Tyr	Asn	Asp	Thr	Ser	Leu
				20					25					30		
	Val	Glu	Asn	His	Leu	Cys	Pro	Ala	Thr	Glu	Gly	Pro	Leu	Met	Ala	Ser
			35					40					45			
	Phe	Lys	Ala	Val	Phe	Val	Pro	Val	Ala	Tyr	Ser	Leu	Ile	Phe	Leu	Leu
		50					55					60				
15	Gly	Val	Ile	Gly	Asn	Val	Leu	Val	Leu	Val	Ile	Leu	Glu	Arg	His	Arg
	65					70					75					80
	Gln	Thr	Arg	Ser	Ser	Thr	Glu	Thr	Phe	Leu	Phe	His	Leu	Ala	Val	Ala
					85					90					95	
20	Asp	Leu	Leu	Leu	Val	Phe	Ile	Leu	Pro	Phe	Ala	Val	Ala	Glu	Gly	Ser
				100					105					110		
	Val	Gly	Trp	Val	Leu	Gly	Thr	Phe	Leu	Cys	Lys	Thr	Val	Ile	Ala	Leu
			115					120					125			
	His	Lys	Val	Asn	Phe	Tyr	Cys	Ser	Ser	Leu	Leu	Leu	Ala	Cys	Ile	Ala
		130					135					140				
25	Val	Asp	Arg	Tyr	Leu	Ala	Ile	Val	His	Ala	Val	His	Ala	Tyr	Arg	His
	145					150					155					160
	Arg	Arg	Leu	Leu	Ser	Ile	His	Ile	Thr	Cys	Gly	Thr	Ile	Trp	Leu	Val
					165					170					175	
30	Gly	Phe	Leu	Leu	Ala	Leu	Pro	Glu	Ile	Leu	Phe	Ala	Lys	Val	Ser	Gln
				180					185					190		
	Gly	His	His	Asn	Asn	Ser	Leu	Pro	Arg	Cys	Thr	Phe	Ser	Gln	Glu	Asn
			195					200					205			
	Gln	Ala	Glu	Thr	His	Ala	Trp	Phe	Thr	Ser	Arg	Phe	Leu	Tyr	His	Val
		210					215					220				
35	Ala	Gly	Phe	Leu	Leu	Pro	Met	Leu	Val	Met	Gly	Trp	Cys	Tyr	Val	Gly
	225					230					235					240
	Val	Val	His	Arg	Leu	Arg	Gln	Ala	Gln	Arg	Arg	Pro	Gln	Arg	Gln	Lys

53

245 250 255

Ala Val Arg Val Ala Ile Leu Val Thr Ser Ile Phe Phe Leu Cys Trp
260 265 270

5 Ser Pro Tyr His Ile Val Ile Phe Leu Asp Thr Leu Ala Arg Leu Lys
275 280 285

Ala Val Asp Asn Thr Cys Lys Leu Asn Gly Ser Leu Pro Val Ala Ile
290 295 300

Thr Met Cys Glu Phe Leu Gly Leu Ala His Cys Cys Leu Asn Pro Met
305 310 315 320

10 Leu Tyr Thr Phe Ala Gly Val Lys Phe Arg Ser Asp Leu Ser Arg Leu
325 330 335

Leu Thr Lys Leu Gly Cys Thr Gly Pro Ala Ser Leu Cys Gln Leu Phe
340 345 350

15 Pro Ser Trp Arg Arg Ser Ser Leu Ser Glu Ser Glu Asn Ala Thr Ser
355 360 365

Leu Thr Thr Phe
370

(68) INFORMATION FOR SEQ ID NO:67:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CAAAGCTTGA AAGCTGCACG GTGCAGAGAC

30

(69) INFORMATION FOR SEQ ID NO:68:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

35 GCGGATCCCG AGTCACACCC TGGCTGGGCC

30

(70) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1128 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

ATGGATGTGA CTTCCAAGC CCGGGGCGTG GGCCTGGAGA TGTACCCAGG CACCGCGCAG 60
CCTGCGGCCC CCAACACCAC CTCCCCGAG CTCAACCTGT CCCACCCGCT CCTGGGCACC 120
10 GCCCTGGCCA ATGGGACAGG TGAGCTCTCG GAGCACCAGC AGTACGTGAT CGGCCTGTTC 180
CTCTCGTGCC TCTACACCAT CTTCTCTTC CCCATCGGCT TTGTGGGCAA CATCCTGATC 240
CTGGTGGTGA ACATCAGCTT CCGCGAGAAG ATGACCATCC CCGACCTGTA CTTTCATCAAC 300
CTGGCGGTGG CGGACCTCAT CCTGGTGGCC GACTCCCTCA TTGAGGTGTT CAACCTGCAC 360
GAGCGGTACT ACGACATCGC CGTCCTGTGC ACCTTCATGT CGCTCTTCCT GCAGGTCAAC 420
15 ATGTACAGCA GCGTCTTCTT CCTCACCTGG ATGAGCTTCG ACCGCTACAT CGCCCTGGCC 480
AGGGCCATGC GCTGCAGCCT GTTCCGCACC AAGCACCAG CCCGGCTGAG CTGTGGCCTC 540
ATCTGGATGG CATCCGTGTC AGCCACGCTG GTGCCCTTCA CCGCCGTGCA CCTGCAGCAC 600
ACCGACGAGG CCTGCTTCTG TTTCGCGGAT GTCCGGGAGG TGCAGTGGCT CGAGGTCACG 660
CTGGGCTTCA TCGTGCCCTT CGCCATCATC GGCCTGTGCT ACTCCCTCAT TGTCCGGGTG 720
20 CTGGTCAGGG CGCACCAGCA CCGTGGGCTG CGGCCCGGC GGCAGAAGGC GCTCCGCATG 780
ATCCTCGCGG TGGTGCTGGT CTTCTTCGTC TGCTGGCTGC CGGAGAACGT CTTTCATCAGC 840
GTGCACCTCC TGCAGCGGAC GCAGCCTGGG GCCGCTCCCT GCAAGCAGTC TTTCCGCCAT 900
GCCACCCCC TCACGGGCCA CATTGTCAAC CTCACGCCT TCTCCAACAG CTGCCTAAAC 960
CCCCTCATCT ACAGCTTCTT CGGGGAGACC TTCAGGGACA AGCTGAGGCT GTACATTGAG 1020
25 CAGAAAACAA ATTTGCCGGC CCTGAACCGC TTCTGTCACG CTGCCCTGAA GGCCGTCATT 1080
CCAGACAGCA CCGAGCAGTC GGATGTGAGG TTCAGCAGTG CCGTGTAG 1128

(71) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: not relevant

30

55.

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

	Met	Asp	Val	Thr	Ser	Gln	Ala	Arg	Gly	Val	Gly	Leu	Glu	Met	Tyr	Pro	
	1				5					10					15		
5	Gly	Thr	Ala	Gln	Pro	Ala	Ala	Pro	Asn	Thr	Thr	Ser	Pro	Glu	Leu	Asn	
				20					25					30			
	Leu	Ser	His	Pro	Leu	Leu	Gly	Thr	Ala	Leu	Ala	Asn	Gly	Thr	Gly	Glu	
			35					40					45				
10	Leu	Ser	Glu	His	Gln	Gln	Tyr	Val	Ile	Gly	Leu	Phe	Leu	Ser	Cys	Leu	
		50					55					60					
	Tyr	Thr	Ile	Phe	Leu	Phe	Pro	Ile	Gly	Phe	Val	Gly	Asn	Ile	Leu	Ile	
	65					70					75				80		
	Leu	Val	Val	Asn	Ile	Ser	Phe	Arg	Glu	Lys	Met	Thr	Ile	Pro	Asp	Leu	
				85						90					95		
15	Tyr	Phe	Ile	Asn	Leu	Ala	Val	Ala	Asp	Leu	Ile	Leu	Val	Ala	Asp	Ser	
				100					105					110			
	Leu	Ile	Glu	Val	Phe	Asn	Leu	His	Glu	Arg	Tyr	Tyr	Asp	Ile	Ala	Val	
		115					120						125				
20	Leu	Cys	Thr	Phe	Met	Ser	Leu	Phe	Leu	Gln	Val	Asn	Met	Tyr	Ser	Ser	
		130					135					140					
	Val	Phe	Phe	Leu	Thr	Trp	Met	Ser	Phe	Asp	Arg	Tyr	Ile	Ala	Leu	Ala	
	145					150					155				160		
	Arg	Ala	Met	Arg	Cys	Ser	Leu	Phe	Arg	Thr	Lys	His	His	Ala	Arg	Leu	
				165						170					175		
25	Ser	Cys	Gly	Leu	Ile	Trp	Met	Ala	Ser	Val	Ser	Ala	Thr	Leu	Val	Pro	
			180					185						190			
	Phe	Thr	Ala	Val	His	Leu	Gln	His	Thr	Asp	Glu	Ala	Cys	Phe	Cys	Phe	
			195				200						205				
30	Ala	Asp	Val	Arg	Glu	Val	Gln	Trp	Leu	Glu	Val	Thr	Leu	Gly	Phe	Ile	
		210					215					220					
	Val	Pro	Phe	Ala	Ile	Ile	Gly	Leu	Cys	Tyr	Ser	Leu	Ile	Val	Arg	Val	
	225					230				235					240		
	Leu	Val	Arg	Ala	His	Arg	His	Arg	Gly	Leu	Arg	Pro	Arg	Arg	Gln	Lys	
				245					250						255		
35	Ala	Leu	Arg	Met	Ile	Leu	Ala	Val	Val	Leu	Val	Phe	Phe	Val	Cys	Trp	
			260						265					270			

56

Leu Pro Glu Asn Val Phe Ile Ser Val His Leu Leu Gln Arg Thr Gln
 275 280 285
 Pro Gly Ala Ala Pro Cys Lys Gln Ser Phe Arg His Ala His Pro Leu
 290 295 300
 5 Thr Gly His Ile Val Asn Leu Thr Ala Phe Ser Asn Ser Cys Leu Asn
 305 310 315 320
 Pro Leu Ile Tyr Ser Phe Leu Gly Glu Thr Phe Arg Asp Lys Leu Arg
 325 330 335
 10 Leu Tyr Ile Glu Gln Lys Thr Asn Leu Pro Ala Leu Asn Arg Phe Cys
 340 345 350
 His Ala Ala Leu Lys Ala Val Ile Pro Asp Ser Thr Glu Gln Ser Asp
 355 360 365
 Val Arg Phe Ser Ser Ala Val
 370 375

15 (72) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 20 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

ACAGAATTCC TGTGTGGTTT TACCGCCCAG

30

(73) INFORMATION FOR SEQ ID NO:72:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

CTCGGATCCA GGCAGAAGAG TCGCCTATGG

30

(74) INFORMATION FOR SEQ ID NO:73:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1137 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

```
ATGGACCTGG GGAAACCAAT GAAAAGCGTG CTGGTGGTGG CTCTCCTTGT CATTTTCCAG      60
5  GTATGCCTGT GTCAAGATGA GGTACGGAC GATTACATCG GAGACAACAC CACAGTGGAC      120
   TACACTTTGT TCGAGTCTTT GTGCTCCAAG AAGGACGTGC GGAAC TTAA AGCCTGGTTC      180
   CTCCTATCA TGTACTCCAT CATTGTGTTT GTGGGCCTAC TGGGCAATGG GCTGGTCGTG      240
   TTGACCTATA TCTATTTCAA GAGGCTCAAG ACCATGACCG ATACCTACCT GCTCAACCTG      300
   GCGGTGGCAG ACATCCTCTT CCTCCTGACC CTTCCCTTCT GGGCCTACAG CGCGGCCAAG      360
10 TCCTGGGTCT TCGGTGTCCA CTTTGTCAAG CTCATCTTTG CCATCTACAA GATGAGCTTC      420
   TTCAGTGGCA TGCTCCTACT TCTTGCATC AGCATTGACC GCTACGTGGC CATCGTCCAG      480
   GCTGTCTCAG CTCACCGCCA CCGTGCCCGC GTCCTTCTCA TCAGCAAGCT GTCCTGTGTG      540
   GGCATCTGGA TACTAGCCAC AGTGCTCTCC ATCCCAGAGC TCCTGTACAG TGACCTCCAG      600
   AGGAGCAGCA GTGAGCAAGC GATGCGATGC TCTCTCATCA CAGAGCATGT GGAGGCCTTT      660
15 ATCACCATCC AGGTGGCCCA GATGGTGATC GGCTTTCTGG TCCCCCTGCT GGCCATGAGC      720
   TTCTGTTACC TTGTCATCAT CCGCACCTG CTCCAGGCAC GCAACTTTGA GCGCAACAAG      780
   GCCATCAAGG TGATCATCGC TGTGGTCGTG GTCTTCATAG TCTTCCAGCT GCCCTACAAT      840
   GGGGTGGTCC TGGCCCAGAC GGTGGCCAAC TTCAACATCA CCAGTAGCAC CTGTGAGCTC      900
   AGTAAGCAAC TCAACATCGC CTACGACGTC ACCTACAGCC TGGCCTGCGT CCGCTGCTGC      960
20 GTCAACCCTT TCTGTACGC CTTCATCGGC GTCAAGTCC GCAACGATCT CTTCAAGCTC     1020
   TTCAAGGACC TGGGCTGCCT CAGCCAGGAG CAGCTCCGGC AGTGGTCTTC CTGTGGGCAC     1080
   ATCCGGCGCT CCTCCATGAG TGTGGAGGCC GAGACCACCA CCACCTTCTC CCCATAG      1137
```

(75) INFORMATION FOR SEQ ID NO:74:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 378 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

	Met	Asp	Leu	Gly	Lys	Pro	Met	Lys	Ser	Val	Leu	Val	Val	Ala	Leu	Leu	
	1				5					10					15		
	Val	Ile	Phe	Gln	Val	Cys	Leu	Cys	Gln	Asp	Glu	Val	Thr	Asp	Asp	Tyr	
				20					25					30			
5	Ile	Gly	Asp	Asn	Thr	Thr	Val	Asp	Tyr	Thr	Leu	Phe	Glu	Ser	Leu	Cys	
		35						40					45				
	Ser	Lys	Lys	Asp	Val	Arg	Asn	Phe	Lys	Ala	Trp	Phe	Leu	Pro	Ile	Met	
		50					55					60					
10	Tyr	Ser	Ile	Ile	Cys	Phe	Val	Gly	Leu	Leu	Gly	Asn	Gly	Leu	Val	Val	
	65				70						75				80		
	Leu	Thr	Tyr	Ile	Tyr	Phe	Lys	Arg	Leu	Lys	Thr	Met	Thr	Asp	Thr	Tyr	
				85						90				95			
	Leu	Leu	Asn	Leu	Ala	Val	Ala	Asp	Ile	Leu	Phe	Leu	Leu	Thr	Leu	Pro	
			100					105						110			
15	Phe	Trp	Ala	Tyr	Ser	Ala	Ala	Lys	Ser	Trp	Val	Phe	Gly	Val	His	Phe	
			115					120					125				
	Cys	Lys	Leu	Ile	Phe	Ala	Ile	Tyr	Lys	Met	Ser	Phe	Phe	Ser	Gly	Met	
		130					135					140					
20	Leu	Leu	Leu	Leu	Cys	Ile	Ser	Ile	Asp	Arg	Tyr	Val	Ala	Ile	Val	Gln	
	145				150						155				160		
	Ala	Val	Ser	Ala	His	Arg	His	Arg	Ala	Arg	Val	Leu	Leu	Ile	Ser	Lys	
				165						170				175			
	Leu	Ser	Cys	Val	Gly	Ile	Trp	Ile	Leu	Ala	Thr	Val	Leu	Ser	Ile	Pro	
			180					185					190				
25	Glu	Leu	Leu	Tyr	Ser	Asp	Leu	Gln	Arg	Ser	Ser	Ser	Glu	Gln	Ala	Met	
		195					200						205				
	Arg	Cys	Ser	Leu	Ile	Thr	Glu	His	Val	Glu	Ala	Phe	Ile	Thr	Ile	Gln	
		210				215						220					
30	Val	Ala	Gln	Met	Val	Ile	Gly	Phe	Leu	Val	Pro	Leu	Leu	Ala	Met	Ser	
	225				230						235				240		
	Phe	Cys	Tyr	Leu	Val	Ile	Ile	Arg	Thr	Leu	Leu	Gln	Ala	Arg	Asn	Phe	
				245						250				255			
	Glu	Arg	Asn	Lys	Ala	Ile	Lys	Val	Ile	Ile	Ala	Val	Val	Val	Val	Phe	
			260					265					270				
35	Ile	Val	Phe	Gln	Leu	Pro	Tyr	Asn	Gly	Val	Val	Leu	Ala	Gln	Thr	Val	
		275						280					285				

59

Ala Asn Phe Asn Ile Thr Ser Ser Thr Cys Glu Leu Ser Lys Gln Leu
 290 295 300

Asn Ile Ala Tyr Asp Val Thr Tyr Ser Leu Ala Cys Val Arg Cys Cys
 305 310 315 320

5 Val Asn Pro Phe Leu Tyr Ala Phe Ile Gly Val Lys Phe Arg Asn Asp
 325 330 335

Leu Phe Lys Leu Phe Lys Asp Leu Gly Cys Leu Ser Gln Glu Gln Leu
 340 345 350

10 Arg Gln Trp Ser Ser Cys Arg His Ile Arg Arg Ser Ser Met Ser Val
 355 360 365

Glu Ala Glu Thr Thr Thr Thr Phe Ser Pro
 370 375

(76) INFORMATION FOR SEQ ID NO:75:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic).

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CTGGAATTCA CCTGGACCAC CACCAATGGA TA

32

(77) INFORMATION FOR SEQ ID NO:76:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

30 CTCGGATCCT GCAAAGTTTG TCATACAGTT

30

(78) INFORMATION FOR SEQ ID NO:77:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1085 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

ATGGATATAC AAATGGCAAA CAATTTTACT CCGCCCTCTG CAACTCCTCA GGGAAATGAC 60
 TGTGACCTCT ATGCACATCA CAGCACGGCC AGGATAGTAA TGCCTCTGCA TTACAGCCTC 120
 GTCTTCATCA TTGGGCTCGT GGGAAACTTA CTAGCCTTGG TCGTCATTGT TCAAAACAGG 180
 5 AAAAAAATCA ACTCTACCAC CCTCTATTCA ACAAATTTGG TGATTTCTGA TATACTTTTT 240
 ACCACGGCTT TGCCTACACG AATAGCCTAC TATGCAATGG GCTTTGACTG GAGAATCGGA 300
 GATGCCTTGT GTAGGATAAC TGCCTAGTGT TTTTACATCA ACACATATGC AGGTGTGAAC 360
 TTTATGACCT GCCTGAGTAT TGACCGCTTC ATTGCTGTGG TGCACCCTCT ACGCTACAAC 420
 AAGATAAAAA GGATTGAACA TGCAAAAGGC GTGTGCATAT TTGTCTGGAT TCTAGTATTT 480
 10 GCTCAGACAC TCCCACTCCT CATCAACCCT ATGTCAAAGC AGGAGGCTGA AAGGATTACA 540
 TGCATGGAGT ATCCAAACTT TGAAGAAACT AAATCTCTTC CCTGGATTCT GCTTGGGGCA 600
 TGTTTCATAG GATATGTACT TCCACTTATA ATCATTCTCA TCTGCTATTC TCAGATCTGC 660
 TGCAAACTCT TCAGAACTGC CAAACAAAAC CCACTCACTG AGAAATCTGG TGTAACAAAA 720
 AAGGCTCTCA ACACAATTAT TCTTATTATT GTTGTGTTTG TTCTCTGTTT CACACCTTAC 780
 15 CATGTTGCAA TTATTCAACA TATGATTAAG AAGCTTCGTT TCTCTAATTT CCTGGAATGT 840
 AGCCAAAGAC ATTCGTTCCA GATTTCTCTG CACTTTACAG TATGCCTGAT GAACTTCAAT 900
 TGCTGCATGG ACCCTTTTAT CTACTTCTTT GCATGTAAAG GGTATAAGAG AAAGGTTATG 960
 AGGATGCTGA AACGGCAAGT CAGTGTATCG ATTTCTAGTG CTGTGAAGTC AGCCCCTGAA 1020
 GAAAATTCAC GTGAAATGAC AGAAACGCAG ATGATGATAC ATTCCAAGTC TTCAAATGGA 1080
 20 AAGTGA 1086

(79) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 361 amino acids
 (B) TYPE: amino acid
 25 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

30 Met Asp Ile Gln Met Ala Asn Asn Phe Thr Pro Pro Ser Ala Thr Pro
 1 5 10 15

Gln Gly Asn Asp Cys Asp Leu Tyr Ala His His Ser Thr Ala Arg Ile
 20 25 30
 Val Met Pro Leu His Tyr Ser Leu Val Phe Ile Ile Gly Leu Val Gly
 35 40 45
 5 Asn Leu Leu Ala Leu Val Val Ile Val Gln Asn Arg Lys Lys Ile Asn
 50 55 60
 Ser Thr Thr Leu Tyr Ser Thr Asn Leu Val Ile Ser Asp Ile Leu Phe
 65 70 75 80
 10 Thr Thr Ala Leu Pro Thr Arg Ile Ala Tyr Tyr Ala Met Gly Phe Asp
 85 90 95
 Trp Arg Ile Gly Asp Ala Leu Cys Arg Ile Thr Ala Leu Val Phe Tyr
 100 105 110
 Ile Asn Thr Tyr Ala Gly Val Asn Phe Met Thr Cys Leu Ser Ile Asp
 115 120 125
 15 Arg Phe Ile Ala Val Val His Pro Leu Arg Tyr Asn Lys Ile Lys Arg
 130 135 140
 Ile Glu His Ala Lys Gly Val Cys Ile Phe Val Trp Ile Leu Val Phe
 145 150 155 160
 20 Ala Gln Thr Leu Pro Leu Leu Ile Asn Pro Met Ser Lys Gln Glu Ala
 165 170 175
 Glu Arg Ile Thr Cys Met Glu Tyr Pro Asn Phe Glu Glu Thr Lys Ser
 180 185 190
 Leu Pro Trp Ile Leu Leu Gly Ala Cys Phe Ile Gly Tyr Val Leu Pro
 195 200 205
 25 Leu Ile Ile Ile Leu Ile Cys Tyr Ser Gln Ile Cys Cys Lys Leu Phe
 210 215 220
 Arg Thr Ala Lys Gln Asn Pro Leu Thr Glu Lys Ser Gly Val Asn Lys
 225 230 235 240
 30 Lys Ala Leu Asn Thr Ile Ile Leu Ile Ile Val Val Phe Val Leu Cys
 245 250 255
 Phe Thr Pro Tyr His Val Ala Ile Ile Gln His Met Ile Lys Lys Leu
 260 265 270
 Arg Phe Ser Asn Phe Leu Glu Cys Ser Gln Arg His Ser Phe Gln Ile
 275 280 285
 35 Ser Leu His Phe Thr Val Cys Leu Met Asn Phe Asn Cys Cys Met Asp
 290 295 300
 Pro Phe Ile Tyr Phe Phe Ala Cys Lys Gly Tyr Lys Arg Lys Val Met

5

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(ii) MOLECULE TYPE: DNA (genomic)

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31

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(ii) MOLECULE TYPE: DNA (genomic)

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(ii) MOLECULE TYPE: DNA (genomic)

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120

CAGAGCCGAT CCAAGAGGGG CACCGAGGAT GAGGAGGCCA AGGGCGTGCA GCAGTATGTG 180
 CCTGAGGAGT GGGCGGAGTA CCCCCGCCCC ATTCACCCTG CTGGCCTGCA GCCAACCAAG 240
 CCCTTGGTGG CCACCAGCCC TAACCCCGAC AAGGATGGGG GCACCCCAAG CAGTGGGCAG 300
 GAACTGAGGG GCAATCTGAC AGGGGCACCA GGGCAGAGGC TACAGATCCA GAACCCCTG 360
 5 TATCCGGTGA CCGAGAGCTC CTACAGTGCC TATGCCATCA TGCTTCTGGC GCTGGTGGTG 420
 TTTGCGGTGG GCATTGTGGG CAACCTGTGC GTCATGTGCA TCGTGTGGCA CAGCTACTAC 480
 CTGAAGAGCG CCTGGAATC CATCCTTGCC AGCCTGGCCC TCTGGGATT TCTGGTCCTC 540
 TTTTCTGCC TCCCTATTGT CATCTTCAAC GAGATCACCA AGCAGAGGCT ACTGGGTGAC 600
 GTTCTCTGTC GTGCCGTGCC CTTTCATGGAG GTCTCCTCTC TGGGAGTCAC GACTTTCAGC 660
 10 CTCTGTGCCC TGGGCATTGA CCGCTTCCAC GTGGCCACCA GCACCCTGCC CAAGGTGAGG 720
 CCCATCGAGC GGTGCCAATC CATCCTGGCC AAGTTGGCTG TCATCTGGGT GGGCTCCATG 780
 ACGCTGGCTG TGCTGAGCT CTTGCTGTGG CAGCTGGCAC AGGAGCCTGC CCCCACCATG 840
 GGCACCCTGG ACTCATGCAT CATGAAACCC TCAGCCAGCC TGCCCAGATC CCTGTATTCA 900
 CTGGTGATGA CCTACCAGAA CGCCCGCATG TGGTGGTACT TTGGCTGCTA CTTCTGCCTG 960
 15 CCCATCCTCT TCACAGTCAC CTGCCAGCTG GTGACATGGC GGGTGCAGAG CCCTCCAGGG 1020
 AGGAAGTCAG AGTGCAGGGC CAGCAAGCAC GAGCAGTGTG AGAGCCAGCT CAACAGCACC 1080
 GTGGTGGGCC TGACCGTGGT CTACGCCTTC TGCACCCTCC CAGAGAACGT CTGCAACATC 1140
 GTGGTGGCCT ACCTCTCCAC CGAGCTGACC CGCCAGACCC TGGACCTCCT GGGCCTCATC 1200
 AACCAGTTCT CCACCTTCTT CAAGGGCGCC ATCACCACAG TGCTGCTCCT TTGCATCTGC 1260
 20 AGGCCGCTGG GCCAGGCCTT CCTGGACTGC TGCTGCTGCT GCTGCTGTGA GGAGTGCAGC 1320
 GGGGCTTCGG AGGCCTCTGC TGCCAATGGG TCGGACAACA AGCTCAAGAC CGAGGTGTCC 1380
 TCTTCCATCT ACTTCCACAA GCCCAGGGAG TCACCCACAC TCCTGCCCCCT GGGCACACCT 1440
 TGCTGA 1446

(83) INFORMATION FOR SEQ ID NO:82:

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 481 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant
- 30 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

	Met	Arg	Trp	Leu	Trp	Pro	Leu	Ala	Val	Ser	Leu	Ala	Val	Ile	Leu	Ala	
	1				5					10					15		
5	Val	Gly	Leu	Ser	Arg	Val	Ser	Gly	Gly	Ala	Pro	Leu	His	Leu	Gly	Arg	
			20					25					30				
	His	Arg	Ala	Glu	Thr	Gln	Glu	Gln	Gln	Ser	Arg	Ser	Lys	Arg	Gly	Thr	
			35					40					45				
	Glu	Asp	Glu	Glu	Ala	Lys	Gly	Val	Gln	Gln	Tyr	Val	Pro	Glu	Glu	Trp	
		50					55					60					
10	Ala	Glu	Tyr	Pro	Arg	Pro	Ile	His	Pro	Ala	Gly	Leu	Gln	Pro	Thr	Lys	
	65					70					75					80	
	Pro	Leu	Val	Ala	Thr	Ser	Pro	Asn	Pro	Asp	Lys	Asp	Gly	Gly	Thr	Pro	
				85					90						95		
15	Asp	Ser	Gly	Gln	Glu	Leu	Arg	Gly	Asn	Leu	Thr	Gly	Ala	Pro	Gly	Gln	
			100					105					110				
	Arg	Leu	Gln	Ile	Gln	Asn	Pro	Leu	Tyr	Pro	Val	Thr	Glu	Ser	Ser	Tyr	
			115				120					125					
	Ser	Ala	Tyr	Ala	Ile	Met	Leu	Leu	Ala	Leu	Val	Val	Phe	Ala	Val	Gly	
		130				135					140						
20	Ile	Val	Gly	Asn	Leu	Ser	Val	Met	Cys	Ile	Val	Trp	His	Ser	Tyr	Tyr	
	145				150					155					160		
	Leu	Lys	Ser	Ala	Trp	Asn	Ser	Ile	Leu	Ala	Ser	Leu	Ala	Leu	Trp	Asp	
			165						170					175			
25	Phe	Leu	Val	Leu	Phe	Phe	Cys	Leu	Pro	Ile	Val	Ile	Phe	Asn	Glu	Ile	
			180					185					190				
	Thr	Lys	Gln	Arg	Leu	Leu	Gly	Asp	Val	Ser	Cys	Arg	Ala	Val	Pro	Phe	
		195					200					205					
	Met	Glu	Val	Ser	Ser	Leu	Gly	Val	Thr	Thr	Phe	Ser	Leu	Cys	Ala	Leu	
		210				215					220						
30	Gly	Ile	Asp	Arg	Phe	His	Val	Ala	Thr	Ser	Thr	Leu	Pro	Lys	Val	Arg	
	225				230					235					240		
	Pro	Ile	Glu	Arg	Cys	Gln	Ser	Ile	Leu	Ala	Lys	Leu	Ala	Val	Ile	Trp	
				245				250				255					
35	Val	Gly	Ser	Met	Thr	Leu	Ala	Val	Pro	Glu	Leu	Leu	Leu	Trp	Gln	Leu	
			260					265				270					
	Ala	Gln	Glu	Pro	Ala	Pro	Thr	Met	Gly	Thr	Leu	Asp	Ser	Cys	Ile	Met	

65

	275	280	285
	Lys Pro Ser Ala Ser Leu	Pro Glu Ser Leu Tyr	Ser Leu Val Met Thr
	290	295	300
5	Tyr Gln Asn Ala Arg Met Trp Trp Tyr Phe Gly Cys Tyr Phe Cys Leu		
	305	310	315 320
	Pro Ile Leu Phe Thr Val Thr Cys Gln Leu Val Thr Trp Arg Val Arg		
	325	330	335
	Gly Pro Pro Gly Arg Lys Ser Glu Cys Arg Ala Ser Lys His Glu Gln		
	340	345	350
10	Cys Glu Ser Gln Leu Asn Ser Thr Val Val Gly Leu Thr Val Val Tyr		
	355	360	365
	Ala Phe Cys Thr Leu Pro Glu Asn Val Cys Asn Ile Val Val Ala Tyr		
	370	375	380
15	Leu Ser Thr Glu Leu Thr Arg Gln Thr Leu Asp Leu Leu Gly Leu Ile		
	385	390	395 400
	Asn Gln Phe Ser Thr Phe Phe Lys Gly Ala Ile Thr Pro Val Leu Leu		
	405	410	415
	Leu Cys Ile Cys Arg Pro Leu Gly Gln Ala Phe Leu Asp Cys Cys Cys		
	420	425	430
20	Cys Cys Cys Cys Glu Glu Cys Gly Gly Ala Ser Glu Ala Ser Ala Ala		
	435	440	445
	Asn Gly Ser Asp Asn Lys Leu Lys Thr Glu Val Ser Ser Ser Ile Tyr		
	450	455	460
25	Phe His Lys Pro Arg Glu Ser Pro Pro Leu Leu Pro Leu Gly Thr Pro		
	465	470	475 480
	Cys		

(84) INFORMATION FOR SEQ ID NO:83:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

ATGTGGAACG CGACGCCAG CG

(85) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

TCATGTATTA ATACTAGATT CT

22

10 (86) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

TACCATGTGG AACGCGACGC CCAGCGAAGA GCCGGGGT

38

(87) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

CGGAATTCAT GTATTAATAC TAGATTCTGT CCAGGCCCG

39

(88) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

67

ATGTGGAACG CGACGCCAG CGAAGAGCCG GGGTTCAACC TCACACTGGC CGACCTGGAC 60
 TGGGATGCTT CCCCCGGCAA CGACTCGCTG GCGGACGAGC TGCTGCAGCT CTTCCCCGCG 120
 CCGCTGCTGG CGGGCGTCAC AGCCACCTGC GTGGCACTCT TCGTGGTGGG TATCGCTGGC 180
 AACCTGCTCA CCATGCTGGT GGTGTCGCGC TTCCGCGAGC TCGCACCAC CACCAACCTC 240
 5 TACCTGTCCA GCATGGCCTT CTCCGATCTG CTCATCTTCC TCTGCATGCC CCTGGACCTC 300
 GTTCGCCTCT GGCAGTACCG GCCCTGGAAC TTCGGCGACC TCCTCTGCAA ACTCTTCCAA 360
 TTCGTCACTG AGAGCTGCAC CTACGCCACG GTGCTCACCA TCACAGCGCT GAGCGTCGAG 420
 CGCTACTTCG CCATCTGCTT CCCACTCCGG GCCAAGGTGG TGGTCACCAA GGGGCGGGTG 480
 AAGCTGGTCA TCTTCGTCAT CTGGGCCGTG GCCTTCTGCA GCGCCGGGCC CATCTTCGTG 540
 10 CTAGTCGGGG TGGAGCACGA GAACGGCACC GACCCTTGGG ACACCAACGA GTGCCGCCCC 600
 ACCGAGTTTG CGGTGCGCTC TGGACTGCTC ACGGTCATGG TGTGGGTGTC CAGCATCTTC 660
 TTCTTCCTTC CTGTCTTCTG TCTCACGGTC CTCTACAGTC TCATCGGCAG GAAGCTGTGG 720
 CGGAGGAGGC GCGGCGATGC TGTCGTGGGT GCCTCGCTCA GGGACCAGAA CCACAAGCAA 780
 ACCGTGAAAA TGCTGGCTGT AGTGGTGTTC GCCTTCATCC TCTGCTGGCT CCCCTTCCAC 840
 15 GTAGGGCGAT ATTTATTTTC CAAATCCTTT GAGCCTGGCT CCTTGGAGAT TGCTCAGATC 900
 AGCCAGTACT GCAACCTCGT GTCCTTTGTC CTCTTCTACC TCAGTGCTGC CATCAACCCC 960
 ATTCTGTACA ACATCATGTC CAAGAAGTAC CGGGTGGCAG TGTTCACTTCT TCTGGGATTTC 1020
 GAACCCCTTCT CCCAGAGAAA GCTCTCCACT CTGAAAGATG AAAGTTCTCG GGCCTGGACA 1080
 GAATCTAGTA TTAATACATG A 1101

20 (89) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 366 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

25 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Met Trp Asn Ala Thr Pro Ser Glu Glu Pro Gly Phe Asn Leu Thr Leu
 1 5 10 15

30 Ala Asp Leu Asp Trp Asp Ala Ser Pro Gly Asn Asp Ser Leu Gly Asp
 20 25 30

Glu Leu Leu Gln Leu Phe Pro Ala Pro Leu Leu Ala Gly Val Thr Ala
 35 40 45
 Thr Cys Val Ala Leu Phe Val Val Gly Ile Ala Gly Asn Leu Leu Thr
 50 55 60
 5 Met Leu Val Val Ser Arg Phe Arg Glu Leu Arg Thr Thr Thr Asn Leu
 65 70 75 80
 Tyr Leu Ser Ser Met Ala Phe Ser Asp Leu Leu Ile Phe Leu Cys Met
 85 90 95
 10 Pro Leu Asp Leu Val Arg Leu Trp Gln Tyr Arg Pro Trp Asn Phe Gly
 100 105 110
 Asp Leu Leu Cys Lys Leu Phe Gln Phe Val Ser Glu Ser Cys Thr Tyr
 115 120 125
 Ala Thr Val Leu Thr Ile Thr Ala Leu Ser Val Glu Arg Tyr Phe Ala
 130 135 140
 15 Ile Cys Phe Pro Leu Arg Ala Lys Val Val Val Thr Lys Gly Arg Val
 145 150 155 160
 Lys Leu Val Ile Phe Val Ile Trp Ala Val Ala Phe Cys Ser Ala Gly
 165 170 175
 20 Pro Ile Phe Val Leu Val Gly Val Glu His Glu Asn Gly Thr Asp Pro
 180 185 190
 Trp Asp Thr Asn Glu Cys Arg Pro Thr Glu Phe Ala Val Arg Ser Gly
 195 200 205
 Leu Leu Thr Val Met Val Trp Val Ser Ser Ile Phe Phe Phe Leu Pro
 210 215 220
 25 Val Phe Cys Leu Thr Val Leu Tyr Ser Leu Ile Gly Arg Lys Leu Trp
 225 230 235 240
 Arg Arg Arg Arg Gly Asp Ala Val Val Gly Ala Ser Leu Arg Asp Gln
 245 250 255
 30 Asn His Lys Gln Thr Val Lys Met Leu Ala Val Val Val Phe Ala Phe
 260 265 270
 Ile Leu Cys Trp Leu Pro Phe His Val Gly Arg Tyr Leu Phe Ser Lys
 275 280 285
 Ser Phe Glu Pro Gly Ser Leu Glu Ile Ala Gln Ile Ser Gln Tyr Cys
 290 295 300
 35 Asn Leu Val Ser Phe Val Leu Phe Tyr Leu Ser Ala Ala Ile Asn Pro
 305 310 315 320
 Ile Leu Tyr Asn Ile Met Ser Lys Lys Tyr Arg Val Ala Val Phe Arg

69

325 330 335

Leu Leu Gly Phe Glu Pro Phe Ser Gln Arg Lys Leu Ser Thr Leu Lys
340 345 350

5 Asp Glu Ser Ser Arg Ala Trp Thr Glu Ser Ser Ile Asn Thr
355 360 365

(90) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GCAAGCTTGT GCCCTCACCA AGCCATGCGA GCC 33

15 (91) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CGGAATTCAG CAATGAGTTC CGACAGAAGC 30

(92) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1842 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

ATGCGAGCCC CGGGCGCGCT TCTCGCCCGC ATGTCGCGGC TACTGCTTCT GCTACTGCTC 60

AAGGTGTCTG CCTCTTCTGC CCTCGGGGTC GCCCCTGCGT CCAGAAACGA AACTTGTCTG 120

GGGGAGAGCT GTGCACCTAC AGTGATCCAG CGCCGCGGCA GGGACGCCTG GGGACCGGGA 180

35 AATTCTGCAA GAGACGTTCT GCGAGCCCGA GCACCCAGGG AGGAGCAGGG GGCAGCGTTT 240

CTTGCGGGAC CCTCCTGGGA CTGCGGGCG GCGCGGGCC GTGACCCGGC TGCAGGCAGA 300
GGGGCGGAGG CGTCGGCAGC CGGACCCCCG GGACCTCCAA CCAGGCCACC TGGCCCCTGG 360
AGGTGGAAG GTGCTCGGGG TCAGGAGCCT TCTGAACTT TGGGGAGAGG GAACCCACG 420
GCCCTCCAGC TCTTCCTTCA GATCTCAGAG GAGGAAGAGA AGGTCCCAG AGGCGCTGGC 480
5 ATTTCCGGGC GTAGCCAGGA GCAGAGTGTG AAGACAGTCC CCGGAGCCAG CGATCTTTTT 540
TACTGGCCAA GGAGAGCCGG GAACTCCAG GTTCCCACC ACAAGCCCCT GTCCAAGACG 600
GCCAATGGAC TGGCGGGGCA CGAAGGGTGG ACAATTGCAC TCCCGGGCCG GGCCTGGCC 660
CAGAATGGAT CCTTGGGTGA AGGAATCCAT GAGCCTGGGG GTCCCCCGCG GGGAAACAGC 720
ACGAACCGGC GTGTGAGACT GAAGAACCCC TTCTACCCGC TGACCCAGGA GTCCTATGGA 780
10 GCCTACGCGG TCATGTGTCT GTCCGTGGTG ATCTTCGGGA CCGGCATCAT TGGCAACCTG 840
GCGGTGATGA GCATCGTGTG CCACAACTAC TACATGCGGA GCATCTCAA CTCCCTCTTG 900
GCCAACCTGG CTTTCTGGGA CTTTCTCATC ATCTTCTTCT GCCTTCCGCT GGTCTCTTC 960
CACGAGCTGA CCAAGAAGTG GCTGCTGGAG GACTTCTCCT GCAAGATCGT GCCCTATATA 1020
GAGGTGCTT CTCTGGGAGT CACCACTTTC ACCTTATGTG CTCTGTGCAT AGACCGCTTC 1080
15 CGTGCTGCCA CCAACGTACA GATGTACTAC GAAATGATCG AAAACTGTTC CTCAACAAC 1140
GCCAACTTG CTGTTATATG GGTGGGAGCT CTATTGTTAG CACTTCCAGA AGTTGTTCTC 1200
CGCCAGCTGA GCAAGGAGGA TTTGGGGTTT AGTGGCCGAG CTCCGGCAGA AAGGTGCATT 1260
ATTAAGATCT CTCCTGATTT ACCAGACACC ATCTATGTTC TAGCCCTCAC CTACGACAGT 1320
GCGAGACTGT GGTGGTATTT TGGCTGTTAC TTTTGTGTC CCACGCTTTT CACCATCACC 1380
20 TGCTCTCTAG TGA CTGCGAG GAAAATCCGC AAAGCAGAGA AAGCCTGTAC CCGAGGGAAT 1440
AAACGGCAGA TTCAACTAGA GAGTCAGATG AACTGTACAG TAGTGGCACT GACCATTTTA 1500
TATGGATTTT GCATTATTCC TGAAAATATC TGCAACATTG TTAGTGCCTA CATGGCTACA 1560
GGGGTTTCAC AGCAGACAAT GGACCTCCTT AATATCATCA GCCAGTTCCT TTTGTTCTTT 1620
AAGTCCTGTG TCACCCCACT CCTCCTTTTC TGTCTCTGCA AACCCTTCAG TCGGGCCTTC 1680
25 ATGGAGTGCT GCTGCTGTTG CTGTGAGGAA TGCATTGAGA AGTCTTCAAC GGTGACCAGT 1740
GATGACAATG ACAACGAGTA CACCACGGAA CTCGAACCTC CGCCTTTCAG TACCATACGC 1800
CGTGAAATGT CCACTTTTGC TTCTGTGCGA ACTCATTGCT GA 1842

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 613 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPCLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Met Arg Ala Pro Gly Ala Leu Leu Ala Arg Met Ser Arg Leu Leu Leu
 1 5 10 15
 Leu Leu Leu Leu Lys Val Ser Ala Ser Ser Ala Leu Gly Val Ala Pro
 20 25 30
 Ala Ser Arg Asn Glu Thr Cys Leu Gly Glu Ser Cys Ala Pro Thr Val
 35 40 45
 Ile Gln Arg Arg Gly Arg Asp Ala Trp Gly Pro Gly Asn Ser Ala Arg
 50 55 60
 Asp Val Leu Arg Ala Arg Ala Pro Arg Glu Glu Gln Gly Ala Ala Phe
 65 70 75 80
 Leu Ala Gly Pro Ser Trp Asp Leu Pro Ala Ala Pro Gly Arg Asp Pro
 85 90 95
 Ala Ala Gly Arg Gly Ala Glu Ala Ser Ala Ala Gly Pro Pro Gly Pro
 100 105 110
 Pro Thr Arg Pro Pro Gly Pro Trp Arg Trp Lys Gly Ala Arg Gly Gln
 115 120 125
 Glu Pro Ser Glu Thr Leu Gly Arg Gly Asn Pro Thr Ala Leu Gln Leu
 130 135 140
 Phe Leu Gln Ile Ser Glu Glu Glu Lys Gly Pro Arg Gly Ala Gly
 145 150 155 160
 Ile Ser Gly Arg Ser Gln Glu Gln Ser Val Lys Thr Val Pro Gly Ala
 165 170 175
 Ser Asp Leu Phe Tyr Trp Pro Arg Arg Ala Gly Lys Leu Gln Gly Ser
 180 185 190
 His His Lys Pro Leu Ser Lys Thr Ala Asn Gly Leu Ala Gly His Glu
 195 200 205
 Gly Trp Thr Ile Ala Leu Pro Gly Arg Ala Leu Ala Gln Asn Gly Ser
 210 215 220
 Leu Gly Glu Gly Ile His Glu Pro Gly Gly Pro Arg Arg Gly Asn Ser
 225 230 235 240

Thr Asn Arg Arg Val Arg Leu Lys Asn Pro Phe Tyr Pro Leu Thr Gln
 245 250 255
 Glu Ser Tyr Gly Ala Tyr Ala Val Met Cys Leu Ser Val Val Ile Phe
 260 265 270
 5 Gly Thr Gly Ile Ile Gly Asn Leu Ala Val Met Ser Ile Val Cys His
 275 280 285
 Asn Tyr Tyr Met Arg Ser Ile Ser Asn Ser Leu Leu Ala Asn Leu Ala
 290 295 300
 10 Phe Trp Asp Phe Leu Ile Ile Phe Phe Cys Leu Pro Leu Val Ile Phe
 305 310 315 320
 His Glu Leu Thr Lys Lys Trp Leu Leu Glu Asp Phe Ser Cys Lys Ile
 325 330 335
 Val Pro Tyr Ile Glu Val Ala Ser Leu Gly Val Thr Thr Phe Thr Leu
 340 345 350
 15 Cys Ala Leu Cys Ile Asp Arg Phe Arg Ala Ala Thr Asn Val Gln Met
 355 360 365
 Tyr Tyr Glu Met Ile Glu Asn Cys Ser Ser Thr Thr Ala Lys Leu Ala
 370 375 380
 20 Val Ile Trp Val Gly Ala Leu Leu Leu Ala Leu Pro Glu Val Val Leu
 385 390 395 400
 Arg Gln Leu Ser Lys Glu Asp Leu Gly Phe Ser Gly Arg Ala Pro Ala
 405 410 415
 Glu Arg Cys Ile Ile Lys Ile Ser Pro Asp Leu Pro Asp Thr Ile Tyr
 420 425 430
 25 Val Leu Ala Leu Thr Tyr Asp Ser Ala Arg Leu Trp Trp Tyr Phe Gly
 435 440 445
 Cys Tyr Phe Cys Leu Pro Thr Leu Phe Thr Ile Thr Cys Ser Leu Val
 450 455 460
 30 Thr Ala Arg Lys Ile Arg Lys Ala Glu Lys Ala Cys Thr Arg Gly Asn
 465 470 475 480
 Lys Arg Gln Ile Gln Leu Glu Ser Gln Met Asn Cys Thr Val Val Ala
 485 490 495
 Leu Thr Ile Leu Tyr Gly Phe Cys Ile Ile Pro Glu Asn Ile Cys Asn
 500 505 510
 35 Ile Val Thr Ala Tyr Met Ala Thr Gly Val Ser Gln Gln Thr Met Asp
 515 520 525
 Leu Leu Asn Ile Ile Ser Gln Phe Leu Leu Phe Phe Lys Ser Cys Val

(94) INFORMATION FOR SEQ ID NO:93:

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

34'

- (95) INFORMATION FOR SEQ ID NO:94:

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

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- 30 (96) INFORMATION FOR SEQ ID NO:95:

- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

```

ATGGTTTTTG CTCACAGAAT GGATAACAGC AAGCCACATT TGATTATTCC TACACTTCTG      60
GTGCCCCCTCC AAAACCGCAG CTGCACTGAA ACAGCCACAC CTCTGCCAAG CCAATACCTG     120
ATGGAATTAA GTGAGGAGCA CAGTTGGATG AGCAACCAAA CAGACCTTCA CTATGTGCTG     180
5  AAACCCGGGG AAGTGGCCAC AGCCAGCATC TTCTTTGGGA TTCTGTGGTT GTTTTCTATC     240
TTCGGCAATT CCCTGGTTTG TTTGGTCATC CATAGGAGTA GGAGGACTCA GTCTACCACC     300
AACTACTTTG TGGTCTCCAT GGCATGTGCT GACCTTCTCA TCAGCGTTGC CAGCACGCCT     360
TTCGTCCTGC TCCAGTTCAC CACTGGAAGG TGGACGCTGG GTAGTGCAAC GTGCAAGGTT     420
GTGCGATATT TTCAATATCT CACTCCAGGT GTCCAGATCT ACGTTCTCCT CTCCATCTGC     480
10 ATAGACCGGT TCTACACCAT CGTCTATCCT CTGAGCTTCA AGGTGTCCAG AGAAAAAGCC     540
AAGAAAATGA TTGCGGCATC GTGGATCTTT GATGCAGGCT TTGTGACCCC TGTGCTCTTT     600
TTCTATGGCT CCAACTGGGA CAGTCATTGT AACTATTTCC TCCCCTCCTC TTGGGAAGGC     660
ACTGCCTACA CTGTCATCCA CTTCTTGGTG GGCTTTGTGA TTCCATCTGT CCTCATAATT     720
TTATTTTACC AAAAGGTCAT AAAATATATT TGGAGAATAG GCACAGATGG CCGAACGGTG     780
15 AGGAGGACAA TGAACATTGT CCCTCGGACA AAAGTGAAAA CTATCAAGAT GTTCCTCATT     840
TTAAATCTGT TGTTTTTGCT CTCCTGGCTG CCTTTTCATG TAGCTCAGCT ATGGCACCCC     900
CATGAACAAG ACTATAAGAA AAGTTCCTT GTTTTCACAG CTATCACATG GATATCCTTT     960
AGTTCTTCAG CCTCTAAACC TACTCTGTAT TCAATTTATA ATGCCAATTT TCGGAGAGGG    1020
ATGAAAGAGA CTTTTTGCAT GTCCTCTATG AAATGTTACC GAAGCAATGC CTATACTATC    1080
20 ACAACAAGTT CAAGGATGGC CAAAAAAAC TACGTTGGCA TTTCAGAAAT CCCTTCCATG    1140
GCCAAACTA TTACCAAAGA CTCGATCTAT GACTCATTTG ACAGAGAAGC CAAGGAAAAA    1200
AAGCTTGCTT GGCCCATTA CTCAAATCCA CCAAATACTT TTGTCTAA                    1248

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(97) INFORMATION FOR SEQ ID NO:96:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 415 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

- 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Met Val Phe Ala His Arg Met Asp Asn Ser Lys Pro His Leu Ile Ile
 1 5 10 15
 Pro Thr Leu Leu Val Pro Leu Gln Asn Arg Ser Cys Thr Glu Thr Ala
 20 25 30
 5 Thr Pro Leu Pro Ser Gln Tyr Leu Met Glu Leu Ser Glu Glu His Ser
 35 40 45
 Trp Met Ser Asn Gln Thr Asp Leu His Tyr Val Leu Lys Pro Gly Glu
 50 55 60
 10 Val Ala Thr Ala Ser Ile Phe Phe Gly Ile Leu Trp Leu Phe Ser Ile
 65 70 75 80
 Phe Gly Asn Ser Leu Val Cys Leu Val Ile His Arg Ser Arg Arg Thr
 85 90 95
 Gln Ser Thr Thr Asn Tyr Phe Val Val Ser Met Ala Cys Ala Asp Leu
 100 105 110
 15 Leu Ile Ser Val Ala Ser Thr Pro Phe Val Leu Leu Gln Phe Thr Thr
 115 120 125
 Gly Arg Trp Thr Leu Gly Ser Ala Thr Cys Lys Val Val Arg Tyr Phe
 130 135 140
 20 Gln Tyr Leu Thr Pro Gly Val Gln Ile Tyr Val Leu Leu Ser Ile Cys
 145 150 155 160
 Ile Asp Arg Phe Tyr Thr Ile Val Tyr Pro Leu Ser Phe Lys Val Ser
 165 170 175
 Arg Glu Lys Ala Lys Lys Met Ile Ala Ala Ser Trp Ile Phe Asp Ala
 180 185 190
 25 Gly Phe Val Thr Pro Val Leu Phe Phe Tyr Gly Ser Asn Trp Asp Ser
 195 200 205
 His Cys Asn Tyr Phe Leu Pro Ser Ser Trp Glu Gly Thr Ala Tyr Thr
 210 215 220
 30 Val Ile His Phe Leu Val Gly Phe Val Ile Pro Ser Val Leu Ile Ile
 225 230 235 240
 Leu Phe Tyr Gln Lys Val Ile Lys Tyr Ile Trp Arg Ile Gly Thr Asp
 245 250 255
 Gly Arg Thr Val Arg Arg Thr Met Asn Ile Val Pro Arg Thr Lys Val
 260 265 270
 35 Lys Thr Ile Lys Met Phe Leu Ile Leu Asn Leu Leu Phe Leu Leu Ser
 275 280 285

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Trp Leu Pro Phe His Val Ala Gln Leu Trp His Pro His Glu Gln Asp
 290 295 300
 Tyr Lys Lys Ser Ser Leu Val Phe Thr Ala Ile Thr Trp Ile Ser Phe
 305 310 315 320
 5 Ser Ser Ser Ala Ser Lys Pro Thr Leu Tyr Ser Ile Tyr Asn Ala Asn
 325 330 335
 Phe Arg Arg Gly Met Lys Glu Thr Phe Cys Met Ser Ser Met Lys Cys
 340 345 350
 10 Tyr Arg Ser Asn Ala Tyr Thr Ile Thr Thr Ser Ser Arg Met Ala Lys
 355 360 365
 Lys Asn Tyr Val Gly Ile Ser Glu Ile Pro Ser Met Ala Lys Thr Ile
 370 375 380
 Thr Lys Asp Ser Ile Tyr Asp Ser Phe Asp Arg Glu Ala Lys Glu Lys
 385 390 395 400
 15 Lys Leu Ala Trp Pro Ile Asn Ser Asn Pro Pro Asn Thr Phe Val
 405 410 415

(98) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 20 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

25 GGAAAGCTTA ACGATCCCCA GGAGCAACAT 30

(99) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 30 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

CTGGGATCCT ACGAGAGCAT TTTTCACACA G 31

35 (100) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1842 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

	ATGGGGCCCA	CCCTAGCGGT	TCCCACCCCC	TATGGCTGTA	TTGGCTGTAA	GCTACCCCAG	60
	CCAGAATACC	CACCGGCTCT	AATCATCTTT	ATGTTCTGCG	CGATGGTTAT	CACCATCGTT	120
	GTAGACCTAA	TCGGCAACTC	CATGGTCATT	TTGGCTGTGA	CGAAGAACAA	GAAGCTCCGG	180
10	AATTCTGGCA	ACATCTTCGT	GGTCAGTCTC	TCTGTGGCCG	ATATGCTGGT	GGCCATCTAC	240
	CCATACCCTT	TGATGCTGCA	TGCCATGTCC	ATTGGGGGCT	GGGATCTGAG	CCAGTTACAG	300
	TGCCAGATGG	TCGGGTTTCT	CACAGGGCTG	AGTGTGGTCG	GCTCCATCTT	CAACATCGTG	360
	GCAATCGCTA	TCAACCGTTA	CTGCTACATC	TGCCACAGCC	TCCAGTACGA	ACGGATCTTC	420
	AGTGTGCGCA	ATACCTGCAT	CTACCTGGTC	ATCACCTGGA	TCATGACCGT	CCTGGCTGTC	480
15	CTGCCCCAACA	TGTACATTGG	CACCATCGAG	TACGATCCTC	GCACCTACAC	CTGCATCTTC	540
	AACTATCTGA	ACAACCCTGT	CTTCACTGTT	ACCATCGTCT	GCATCCACTT	CGTCTTCCCT	600
	CTCCTCATCG	TGGGTTTCTG	CTACGTGAGG	ATCTGGACCA	AAGTGCTGGC	GGCCCGTGAC	660
	CCTGCAGGGC	AGAATCCTGA	CAACCAACTT	GCTGAGGTTT	GCAATTTTCT	AACCATGTTT	720
	GTGATCTTCC	TCCTCTTTGC	AGTGTGCTGG	TGCCCTATCA	ACGTGCTCAC	TGTCTTGGTG	780
20	GCTGTGAGTC	CGAAGGAGAT	GGCAGGCAAG	ATCCCCAACT	GGCTTTATCT	TGCAGCCTAC	840
	TTCATAGCCT	ACTTCAACAG	CTGCCTCAAC	GCTGTGATCT	ACGGGCTCCT	CAATGAGAAT	900
	TTCCGAAGAG	AATACTGGAC	CATCTTCCAT	GCTATGCGGC	ACCCTATCAT	ATTCTTCCCT	960
	GGCCTCATCA	GTGATATTCT	TGAGATGCAG	GAGGCCCCGT	CCCTGGCCCC	CGCCCGTGCC	1020
	CATGCTCGCG	ACCAAGCTCG	TGAACAAGAC	CGTGCCCATG	CCTGTCCTGC	TGTGGAGGAA	1080
25	ACCCCGATGA	ATGTCCGGAA	TGTTCCATTA	CCTGGTGATG	CTGCAGCTGG	CCACCCCGAC	1140
	CGTGCCTCTG	GCCACCCTAA	GCCCCATTCC	AGATCCTCCT	CTGCCTATCG	CAAATCTGCC	1200
	TCTACCCACC	ACAAGTCTGT	CTTTAGCCAC	TCCAAGGCTG	CCTCTGGTCA	CCTCAAGCCT	1260
	GTCTCTGGCC	ACTCCAAGCC	TGCCTCTGGT	CACCCCAAGT	CTGCCACTGT	CTACCCTAAG	1320
	CCTGCCTCTG	TCCATTTCAA	GGGTGACTCT	GTCCATTTCA	AGGGTGACTC	TGTCCATTTC	1380

AAGCCTGACT CTGTTTCATT CAAGCCTGCT TCCAGCAACC CCAAGCCCAT CACTGGCCAC 1440
 CATGTCTCTG CTGGCAGCCA CTCCAAGTCT GCCTTCAGTG CTGCCACCAG CCACCCTAAA 1500
 CCCATCAAGC CAGCTACCAG CCATGCTGAG CCCACCACTG CTGACTATCC CAAGCCTGCC 1560
 ACTACCAGCC ACCCTAAGCC CGCTGCTGCT GACAACCCTG AGCTCTCTGC CTCCCATTGC 1620
 5 CCCGAGATCC CTGCCATTGC CCACCCTGTG TCTGACGACA GTGACCTCCC TGAGTCGGCC 1680
 TCTAGCCCTG CCGCTGGGCC CACCAAGCCT GCTGCCAGCC AGCTGGAGTC TGACACCATC 1740
 GCTGACCTTC CTGACCCTAC TGTAGTCACT ACCAGTACCA ATGATTACCA TGATGTCGTG 1800
 GTTGTGATG TTGAAGATGA TCCTGATGAA ATGGCTGTGT GA 1842

(101) INFORMATION FOR SEQ ID NO:100:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 613 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

- 15 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Met Gly Pro Thr Leu Ala Val Pro Thr Pro Tyr Gly Cys Ile Gly Cys
 1 5 10 15
 Lys Leu Pro Gln Pro Glu Tyr Pro Pro Ala Leu Ile Ile Phe Met Phe
 20 20 25 30
 Cys Ala Met Val Ile Thr Ile Val Val Asp Leu Ile Gly Asn Ser Met
 35 40 45
 Val Ile Leu Ala Val Thr Lys Asn Lys Lys Leu Arg Asn Ser Gly Asn
 50 55 60
 25 Ile Phe Val Val Ser Leu Ser Val Ala Asp Met Leu Val Ala Ile Tyr
 65 70 75 80
 Pro Tyr Pro Leu Met Leu His Ala Met Ser Ile Gly Gly Trp Asp Leu
 85 90 95
 Ser Gln Leu Gln Cys Gln Met Val Gly Phe Ile Thr Gly Leu Ser Val
 30 100 105 110
 Val Gly Ser Ile Phe Asn Ile Val Ala Ile Ala Ile Asn Arg Tyr Cys
 115 120 125
 Tyr Ile Cys His Ser Leu Gln Tyr Glu Arg Ile Phe Ser Val Arg Asn
 130 135 140

Thr Cys Ile Tyr Leu Val Ile Thr Trp Ile Met Thr Val Leu Ala Val
 145 150 155 160
 Leu Pro Asn Met Tyr Ile Gly Thr Ile Glu Tyr Asp Pro Arg Thr Tyr
 165 170 175
 5 Thr Cys Ile Phe Asn Tyr Leu Asn Asn Pro Val Phe Thr Val Thr Ile
 180 185 190
 Val Cys Ile His Phe Val Leu Pro Leu Leu Ile Val Gly Phe Cys Tyr
 195 200 205
 10 Val Arg Ile Trp Thr Lys Val Leu Ala Ala Arg Asp Pro Ala Gly Gln
 210 215 220
 Asn Pro Asp Asn Gln Leu Ala Glu Val Arg Asn Phe Leu Thr Met Phe
 225 230 235 240
 Val Ile Phe Leu Leu Phe Ala Val Cys Trp Cys Pro Ile Asn Val Leu
 245 250 255
 15 Thr Val Leu Val Ala Val Ser Pro Lys Glu Met Ala Gly Lys Ile Pro
 260 265 270
 Asn Trp Leu Tyr Leu Ala Ala Tyr Phe Ile Ala Tyr Phe Asn Ser Cys
 275 280 285
 20 Leu Asn Ala Val Ile Tyr Gly Leu Leu Asn Glu Asn Phe Arg Arg Glu
 290 295 300
 Tyr Trp Thr Ile Phe His Ala Met Arg His Pro Ile Ile Phe Phe Pro
 305 310 315 320
 Gly Leu Ile Ser Asp Ile Arg Glu Met Gln Glu Ala Arg Thr Leu Ala
 325 330 335
 25 Arg Ala Arg Ala His Ala Arg Asp Gln Ala Arg Glu Gln Asp Arg Ala
 340 345 350
 His Ala Cys Pro Ala Val Glu Glu Thr Pro Met Asn Val Arg Asn Val
 355 360 365
 30 Pro Leu Pro Gly Asp Ala Ala Ala Gly His Pro Asp Arg Ala Ser Gly
 370 375 380
 His Pro Lys Pro His Ser Arg Ser Ser Ser Ala Tyr Arg Lys Ser Ala
 385 390 395 400
 Ser Thr His His Lys Ser Val Phe Ser His Ser Lys Ala Ala Ser Gly
 405 410 415
 35 His Leu Lys Pro Val Ser Gly His Ser Lys Pro Ala Ser Gly His Pro
 420 425 430
 Lys Ser Ala Thr Val Tyr Pro Lys Pro Ala Ser Val His Phe Lys Gly

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	435	440	445
	Asp Ser Val His Phe Lys Gly Asp Ser Val His Phe Lys Pro Asp Ser		
	450	455	460
5	Val His Phe Lys Pro Ala Ser Ser Asn Pro Lys Pro Ile Thr Gly His		
	465	470	475 480
	His Val Ser Ala Gly Ser His Ser Lys Ser Ala Phe Ser Ala Ala Thr		
		485	490 495
	Ser His Pro Lys Pro Ile Lys Pro Ala Thr Ser His Ala Glu Pro Thr		
		500	505 510
10	Thr Ala Asp Tyr Pro Lys Pro Ala Thr Thr Ser His Pro Lys Pro Ala		
		515	520 525
	Ala Ala Asp Asn Pro Glu Leu Ser Ala Ser His Cys Pro Glu Ile Pro		
		530	535 540
15	Ala Ile Ala His Pro Val Ser Asp Asp Ser Asp Leu Pro Glu Ser Ala		
		545	550 555 560
	Ser Ser Pro Ala Ala Gly Pro Thr Lys Pro Ala Ala Ser Gln Leu Glu		
		565	570 575
	Ser Asp Thr Ile Ala Asp Leu Pro Asp Pro Thr Val Val Thr Thr Ser		
		580	585 590
20	Thr Asn Asp Tyr His Asp Val Val Val Val Asp Val Glu Asp Asp Pro		
		595	600 605
	Asp Glu Met Ala Val		
	610		

(102) INFORMATION FOR SEQ ID NO:101:

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- 30 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TCCAAGCTTC GCCATGGGAC ATAACGGGAG CT

32

(103) INFORMATION FOR SEQ ID NO:102:

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

CGTGAATTCC AAGAATTAC AATCCTTGCT

30

5 (104) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1548 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

10 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

	ATGGGACATA ACGGGAGCTG GATCTCTCCA AATGCCAGCG AGCCGCACAA CGCGTCCGGC	60
	GCCGAGGCTG CGGGGTGAA CCGCAGCGCG CTCGGGGAGT TCGGCGAGGC GCAGCTGTAC	120
15	CGCCAGTTCA CCACCACCGT GCAGGTCGTC ATCTTCATAG GCTCGCTGCT CGGAAACTTC	180
	ATGGTGTTAT GGTCAACTTG CCGCACAACC GTGTTCAAAT CTGTCACCAA CAGGTTTCATT	240
	AAAAACCTGG CCTGCTCGGG GATTTGTGCC AGCCTGGTCT GTGTGCCCTT CGACATCATC	300
	CTCAGACCA GTCTCACTG TTGCTGGTGG ATCTACACCA TGCTCTTCTG CAAGGTCGTC	360
	AAATTTTTGC ACAAAGTATT CTGCTCTGTG ACCATCCTCA GCTTCCCTGC TATTGCTTTG	420
20	GACAGGTA CTCTAGTCCT CTATCCACTG GAGAGGAAAA TATCTGATGC CAAGTCCCGT	480
	GAACTGGTGA TGTACATCTG GGCCCATGCA GTGGTGGCCA GTGTCCCTGT GTTTGCAGTA	540
	ACCAATGTGG CTGACATCTA TGCCACGTCC ACCTGCACGG AAGTCTGGAG CAACTCCTTG	600
	GGCCACCTGG TGTACGTTCT GGTGTATAAC ATCACCACGG TCATTGTGCC TGTGGTGGTG	660
	GTGTTCTCT TCTTGATACT GATCCGACGG GCCCTGAGTG CCAGCCAGAA GAAGAAGGTC	720
25	ATCATAGCAG CGCTCCGGAC CCCACAGAAC ACCATCTCTA TTCCCTATGC CTCCCAGCGG	780
	GAGGCCGAGC TGCACGCCAC CCTGCTCTCC ATGGTGATGG TCTTCATCTT GTGTAGCGTG	840
	CCCTATGCCA CCCTGGTCGT CTACCAGACT GTGCTCAATG TCCCTGACAC TTCCGTCTTC	900
	TTGCTGCTCA CTGCTGTTTG GCTGCCCAA GTCTCCCTGC TGGCAAACCC TGTTCTCTTT	960
	CTTACTGTGA ACAAATCTGT CCGCAAGTGC TTGATAGGGA CCCTGGTGCA ACTACACCAC	1020
30	CGGTACAGTC GCCGTAATGT GGTCAGTACA GGGAGTGGCA TGGCTGAGGC CAGCCTGGAA	1080

CCCAGCATAC GCTCGGGTAG CCAGCTCCTG GAGATGTTCC ACATTGGGCA GCAGCAGATC 1140
 TTTAAGCCCA CAGAGGATGA GGAAGAGAGT GAGGCCAAGT ACATTGGCTC AGCTGACTTC 1200
 CAGGCCAAGG AGATATTTAG CACCTGCCTC GAGGGAGAGC AGGGGCCACA GTTTGCGCCC 1260
 TCTGCCCCAC CCCTGAGCAC AGTGGACTCT GTATCCCAGG TGGCACCGGC AGCCCCTGTG 1320
 5 GAACCTGAAA CATTCCCTGA TAAGTATTCC CTGCAGTTTG GCTTTGGGCC TTTTGAGTTG 1380
 CCTCCTCAGT GGCTCTCAGA GACCCGAAAC AGCAAGAAGC GGCTGCTTCC CCCCTTGGGC 1440
 AACACCCAG AAGAGCTGAT CCAGACAAAG GTGCCCAAGG TAGGCAGGGT GGAGCGGAAG 1500
 ATGAGCAGAA ACAATAAAGT GAGCATTTTT CCAAAGGTGG ATTCCTAG 1548

(105) INFORMATION FOR SEQ ID NO:104:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 515 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

15 (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Met	Gly	His	Asn	Gly	Ser	Trp	Ile	Ser	Pro	Asn	Ala	Ser	Glu	Pro	His	1	5	10	15
Asn	Ala	Ser	Gly	Ala	Glu	Ala	Ala	Gly	Val	Asn	Arg	Ser	Ala	Leu	Gly	20	25	30	
Glu	Phe	Gly	Glu	Ala	Gln	Leu	Tyr	Arg	Gln	Phe	Thr	Thr	Thr	Val	Gln	35	40	45	
Val	Val	Ile	Phe	Ile	Gly	Ser	Leu	Leu	Gly	Asn	Phe	Met	Val	Leu	Trp	50	55	60	
Ser	Thr	Cys	Arg	Thr	Thr	Val	Phe	Lys	Ser	Val	Thr	Asn	Arg	Phe	Ile	65	70	75	80
Lys	Asn	Leu	Ala	Cys	Ser	Gly	Ile	Cys	Ala	Ser	Leu	Val	Cys	Val	Pro	85	90	95	
Phe	Asp	Ile	Ile	Leu	Ser	Thr	Ser	Pro	His	Cys	Cys	Trp	Trp	Ile	Tyr	100	105	110	
Thr	Met	Leu	Phe	Cys	Lys	Val	Val	Lys	Phe	Leu	His	Lys	Val	Phe	Cys	115	120	125	
Ser	Val	Thr	Ile	Leu	Ser	Phe	Pro	Ala	Ile	Ala	Leu	Asp	Arg	Tyr	Tyr	130	135	140	

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	Ser Val Leu Tyr Pro Leu Glu Arg Lys Ile Ser Asp Ala Lys Ser Arg	145	150	155	160
	Glu Leu Val Met Tyr Ile Trp Ala His Ala Val Val Ala Ser Val Pro	165	170	175	
5	Val Phe Ala Val Thr Asn Val Ala Asp Ile Tyr Ala Thr Ser Thr Cys	180	185	190	
	Thr Glu Val Trp Ser Asn Ser Leu Gly His Leu Val Tyr Val Leu Val	195	200	205	
10	Tyr Asn Ile Thr Thr Val Ile Val Pro Val Val Val Val Phe Leu Phe	210	215	220	
	Leu Ile Leu Ile Arg Arg Ala Leu Ser Ala Ser Gln Lys Lys Lys Val	225	230	235	240
	Ile Ile Ala Ala Leu Arg Thr Pro Gln Asn Thr Ile Ser Ile Pro Tyr	245	250	255	
15	Ala Ser Gln Arg Glu Ala Glu Leu His Ala Thr Leu Leu Ser Met Val	260	265	270	
	Met Val Phe Ile Leu Cys Ser Val Pro Tyr Ala Thr Leu Val Val Tyr	275	280	285	
20	Gln Thr Val Leu Asn Val Pro Asp Thr Ser Val Phe Leu Leu Leu Thr	290	295	300	
	Ala Val Trp Leu Pro Lys Val Ser Leu Leu Ala Asn Pro Val Leu Phe	305	310	315	320
	Leu Thr Val Asn Lys Ser Val Arg Lys Cys Leu Ile Gly Thr Leu Val	325	330	335	
25	Gln Leu His His Arg Tyr Ser Arg Arg Asn Val Val Ser Thr Gly Ser	340	345	350	
	Gly Met Ala Glu Ala Ser Leu Glu Pro Ser Ile Arg Ser Gly Ser Gln	355	360	365	
30	Leu Leu Glu Met Phe His Ile Gly Gln Gln Gln Ile Phe Lys Pro Thr	370	375	380	
	Glu Asp Glu Glu Glu Ser Glu Ala Lys Tyr Ile Gly Ser Ala Asp Phe	385	390	395	400
	Gln Ala Lys Glu Ile Phe Ser Thr Cys Leu Glu Gly Glu Gln Gly Pro	405	410	415	
35	Gln Phe Ala Pro Ser Ala Pro Pro Leu Ser Thr Val Asp Ser Val Ser	420	425	430	
	Gln Val Ala Pro Ala Ala Pro Val Glu Pro Glu Thr Phe Pro Asp Lys				

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435 440 445
 Tyr Ser Leu Gln Phe Gly Phe Gly Pro Phe Glu Leu Pro Pro Gln Trp
 450 455 460
 5 Leu Ser Glu Thr Arg Asn Ser Lys Lys Arg Leu Leu Pro Pro Leu Gly
 465 470 475 480
 Asn Thr Pro Glu Glu Leu Ile Gln Thr Lys Val Pro Lys Val Gly Arg
 485 490 495
 Val Glu Arg Lys Met Ser Arg Asn Asn Lys Val Ser Ile Phe Pro Lys
 500 505 510
 10 Val Asp Ser
 515

(106) INFORMATION FOR SEQ ID NO:105:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

20 GGAGAATTCA CTAGGCGAGG CGCTCCATC

29

(107) INFORMATION FOR SEQ ID NO:106:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GGAGGATCCA GGAAACCTTA GGCCGAGTCC

30

30 (108) INFORMATION FOR SEQ ID NO:107:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1164 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

ATGAATCGGC ACCATCTGCA GGATCACTTT CTGGAAATAG ACAAGAAGAA CTGCTGTGTG 60
TTCCGAGATG ACTTCATTGC CAAGGTGTTG CCGCCGGTGT TGGGGCTGGA GTTTATCTTT 120
GGGCTTCTGG GCAATGGCCT TGCCCTGTGG ATTTTCTGTT TCCACCTCAA GTCCTGGAAA 180
5 TCCAGCCGGA TTTTCTGTG CAACCTGGCA GTAGCTGACT TTCTACTGAT CATCTGCCTG 240
CCGTTCGTGA TGGACTACTA TGTGCGGCGT TCAGACTGGA ACTTTGGGGA CATCCCTTGC 300
CGGCTGGTGC TCTTCATGTT TGCCATGAAC CGCCAGGGCA GCATCATCTT CCTCACGGTG 360
GTGGCGGTAG ACAGGTATTT CCGGGTGGTC CATCCCCACC ACGCCCTGAA CAAGATCTCC 420
AATTGGACAG CAGCCATCAT CTCTGCCTT CTGTGGGGCA TCACTGTTGG CCTAACAGTC 480
10 CACCTCCTGA AGAAGAAGTT GCTGATCCAG AATGGCCCTG CAAATGTGTG CATCAGCTTC 540
AGCATCTGCC ATACCTTCCG GTGGCAGGAA GCTATGTTCC TCCTGGAGTT CCTCCTGCCC 600
CTGGGCATCA TCCTGTTCTG CTCAGCCAGA ATTATCTGGA GCCTGCGGCA GAGACAAATG 660
GACCGGCATG CCAAGATCAA GAGAGCCATC ACCTTCATCA TGGTGGTGGC CATCGTCTTT 720
GTCATCTGCT TCCTTCCCAG CGTGGTTGTG CGGATCCGCA TCTTCTGGCT CCTGCACACT 780
15 TCGGGCACGC AGAATTGTGA AGTGTACCGC TCGGTGGACC TGGCGTTCTT TATCACTCTC 840
AGCTTCACCT ACATGAACAG CATGCTGGAC CCCGTGGTGT ACTACTTCTC CAGCCCATCC 900
TTTCCCAACT TCTTCTCCAC TTTGATCAAC CGCTGCCTCC AGAGGAAGAT GACAGGTGAG 960
CCAGATAATA ACCGCAGCAC GAGCGTCGAG CTCACAGGGG ACCCCAACAA AACCAGAGGC 1020
GCTCCAGAGG CGTTAATGGC CAACTCCGGT GAGCCATGGA GCCCTCTTA TCTGGGCCCCA 1080
20 ACCTCAAATA ACCATTCCAA GAAGGGACAT TGTCACCAAG AACCAGCATC TCTGGAGAAA 1140
CAGTTGGGCT GTGCATCGA GTAA 1164

(109) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
25 (A) LENGTH: 387 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

30 Met Asn Arg His His Leu Gln Asp His Phe Leu Glu Ile Asp Lys Lys

86

	1		5		10		15									
	Asn	Cys	Cys	Val	Phe	Arg	Asp	Asp	Phe	Ile	Ala	Lys	Val	Leu	Pro	Pro
				20					25					30		
5	Val	Leu	Gly	Leu	Glu	Phe	Ile	Phe	Gly	Leu	Leu	Gly	Asn	Gly	Leu	Ala
			35					40					45			
	Leu	Trp	Ile	Phe	Cys	Phe	His	Leu	Lys	Ser	Trp	Lys	Ser	Ser	Arg	Ile
		50					55					60				
	Phe	Leu	Phe	Asn	Leu	Ala	Val	Ala	Asp	Phe	Leu	Leu	Ile	Ile	Cys	Leu
	65					70					75				80	
10	Pro	Phe	Val	Met	Asp	Tyr	Tyr	Val	Arg	Arg	Ser	Asp	Trp	Asn	Phe	Gly
					85					90					95	
	Asp	Ile	Pro	Cys	Arg	Leu	Val	Leu	Phe	Met	Phe	Ala	Met	Asn	Arg	Gln
				100					105					110		
15	Gly	Ser	Ile	Ile	Phe	Leu	Thr	Val	Val	Ala	Val	Asp	Arg	Tyr	Phe	Arg
			115					120					125			
	Val	Val	His	Pro	His	His	Ala	Leu	Asn	Lys	Ile	Ser	Asn	Trp	Thr	Ala
			130				135						140			
	Ala	Ile	Ile	Ser	Cys	Leu	Leu	Trp	Gly	Ile	Thr	Val	Gly	Leu	Thr	Val
	145					150					155				160	
20	His	Leu	Leu	Lys	Lys	Lys	Leu	Leu	Ile	Gln	Asn	Gly	Pro	Ala	Asn	Val
				165						170					175	
	Cys	Ile	Ser	Phe	Ser	Ile	Cys	His	Thr	Phe	Arg	Trp	His	Glu	Ala	Met
			180						185					190		
25	Phe	Leu	Leu	Glu	Phe	Leu	Leu	Pro	Leu	Gly	Ile	Ile	Leu	Phe	Cys	Ser
			195					200					205			
	Ala	Arg	Ile	Ile	Trp	Ser	Leu	Arg	Gln	Arg	Gln	Met	Asp	Arg	His	Ala
	210						215					220				
	Lys	Ile	Lys	Arg	Ala	Ile	Thr	Phe	Ile	Met	Val	Val	Ala	Ile	Val	Phe
	225					230					235				240	
30	Val	Ile	Cys	Phe	Leu	Pro	Ser	Val	Val	Val	Arg	Ile	Arg	Ile	Phe	Trp
				245						250				255		
	Leu	Leu	His	Thr	Ser	Gly	Thr	Gln	Asn	Cys	Glu	Val	Tyr	Arg	Ser	Val
			260					265						270		
35	Asp	Leu	Ala	Phe	Phe	Ile	Thr	Leu	Ser	Phe	Thr	Tyr	Met	Asn	Ser	Met
		275						280					285			
	Leu	Asp	Pro	Val	Val	Tyr	Tyr	Phe	Ser	Ser	Pro	Ser	Phe	Pro	Asn	Phe
	290						295						300			

87

Phe Ser Thr Leu Ile Asn Arg Cys Leu Gln Arg Lys Met Thr Gly Glu
305 310 315 320

Pro Asp Asn Asn Arg Ser Thr Ser Val Glu Leu Thr Gly Asp Pro Asn
325 330 335

5 Lys Thr Arg Gly Ala Pro Glu Ala Leu Met Ala Asn Ser Gly Glu Pro
340 345 350

Trp Ser Pro Ser Tyr Leu Gly Pro Thr Ser Asn Asn His Ser Lys Lys
355 360 365

10 Gly His Cys His Gln Glu Pro Ala Ser Leu Glu Lys Gln Leu Gly Cys
370 375 380

Cys Ile Glu
385

(110) INFORMATION FOR SEQ ID NO:109:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- 20 (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

ACCATGGCTT GCAATGGCAG TCGGCCAGG GGGCACT

37

(111) INFORMATION FOR SEQ ID NO:110:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- 30 (iv) ANTI-SENSE: YES
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

CGACCAGGAC AAACAGCATC TTGGTCACTT GTCTCCGGC

39

(112) INFORMATION FOR SEQ ID NO:111:

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

5 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

GACCAAGATG CTGTTTGTCC TGGTCGTGGT GTTTGGCAT 39

(113) INFORMATION FOR SEQ ID NO:112:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

15 (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

CGGAATTCAG GATGGATCGG TCTCTTGCTG CGCCT 35

(114) INFORMATION FOR SEQ ID NO:113:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1212 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

ATGGCTTGCA ATGGCAGTGC GGCCAGGGGG CACTTTGACC CTGAGGACTT GAACCTGACT 60

GACGAGGCAC TGAGACTCAA GTACCTGGGG CCCCAGCAGA CAGAGCTGTT CATGCCCATC 120

TGTGCCACAT ACCTGCTGAT CTTCTGTTGG GCGCTGTGG GCAATGGGCT GACCTGTCTG 180

GTCATCCTGC GCCACAAGGC CATGCGCAGC CCTACCAACT ACTACCTCTT CAGCCTGGCC 240

30 GTGTCGGACC TGCTGGTGCT GCTGGTGGGC CTGCCCCTGG AGCTCTATGA GATGTGGCAC 300

AACTACCCCT TCCTGCTGGG CGTTGGTGGC TGCTATTTCC GCACGCTACT GTTTGAGATG 360

GTCTGCCTGG CCTCAGTGCT CAACGTCAGT GCCCTGAGCG TGAACGCTA TGTGGCCGTG 420

GTGCACCCAC TCCAGGCCAG GTCCATGGTG ACGCGGGCCC ATGTGCGCCG AGTGCTTGGG 480

GCCGTCTGGG GTCTTGCCAT GCTCTGCTCC CTGCCCAACA CCAGCCTGCA CGGCATCCGG 540
 CAGCTGCACG TGCCCTGCCG GGGCCCAGTG CCAGACTCAG CTGTTTGCAT GCTGGTCCGC 600
 CCACGGGCCC TCTACAACAT GGTAGTGCAG ACCACCGCGC TGCTCTTCTT CTGCCTGCCC 660
 ATGGCCATCA TGAGCGTGCT CTACCTGCTC ATTGGGCTGC GACTGCGGCG GGAGAGGCTG 720
 5 CTGCTCATGC AGGAGGCCAA GGGCAGGGGC TCTGCAGCAG CCAGGTCCAG ATACACCTGC 780
 AGGCTCCAGC AGCACGATCG GGGCCGGAGA CAAGTGACCA AGATGCTGTT TGTCTGGTC 840
 GTGGTGTTTG GCATCTGCTG GGCCCCGTTT CACGCCGACC GCGTCATGTG GAGCGTCGTG 900
 TCACAGTGGA CAGATGGCCT GCACCTGGCC TTCCAGCAGC TGCACGTCAT CTCCGGCATC 960
 TTCTTCTACC TGGGCTCGGC GGCCAACCCC GTGCTCTATA GCCTCATGTC CAGCCGCTTC 1020
 10 CGAGAGACCT TCCAGGAGGC CCTGTGCCTC GGGGCCTGCT GCCATCGCCT CAGACCCCGC 1080
 CACAGCTCCC ACAGCCTCAG CAGGATGACC ACAGGCAGCA CCCTGTGTGA TGTGGGCTCC 1140
 CTGGGCAGCT GGGTCCACCC CCTGGCTGGG AACGATGGCC CAGAGGCGCA GCAAGAGACC 1200
 GATCCATCCT GA 1212

(115) INFORMATION FOR SEQ ID NO:114:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 403 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant
- 20 (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:
- | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Cys | Asn | Gly | Ser | Ala | Ala | Arg | Gly | His | Phe | Asp | Pro | Glu | Asp |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Leu | Asn | Leu | Thr | Asp | Glu | Ala | Leu | Arg | Leu | Lys | Tyr | Leu | Gly | Pro | Gln |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Gln | Thr | Glu | Leu | Phe | Met | Pro | Ile | Cys | Ala | Thr | Tyr | Leu | Leu | Ile | Phe |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Val | Val | Gly | Ala | Val | Gly | Asn | Gly | Leu | Thr | Cys | Leu | Val | Ile | Leu | Arg |
| | 50 | | | | 55 | | | | | | 60 | | | | |
| His | Lys | Ala | Met | Arg | Thr | Pro | Thr | Asn | Tyr | Tyr | Leu | Phe | Ser | Leu | Ala |
| 65 | | | | 70 | | | | | 75 | | | | | 80 | |
| Val | Ser | Asp | Leu | Leu | Val | Leu | Leu | Val | Gly | Leu | Pro | Leu | Glu | Leu | Tyr |
| | | | 85 | | | | | 90 | | | | | 95 | | |

90

Glu Met Trp His Asn Tyr Pro Phe Leu Leu Gly Val Gly Gly Cys Tyr
 100 105 110
 Phe Arg Thr Leu Leu Phe Glu Met Val Cys Leu Ala Ser Val Leu Asn
 115 120 125
 5 Val Thr Ala Leu Ser Val Glu Arg Tyr Val Ala Val Val His Pro Leu
 130 135 140
 Gln Ala Arg Ser Met Val Thr Arg Ala His Val Arg Arg Val Leu Gly
 145 150 155 160
 10 Ala Val Trp Gly Leu Ala Met Leu Cys Ser Leu Pro Asn Thr Ser Leu
 165 170 175
 His Gly Ile Arg Gln Leu His Val Pro Cys Arg Gly Pro Val Pro Asp
 180 185 190
 Ser Ala Val Cys Met Leu Val Arg Pro Arg Ala Leu Tyr Asn Met Val
 195 200 205
 15 Val Gln Thr Thr Ala Leu Leu Phe Phe Cys Leu Pro Met Ala Ile Met
 210 215 220
 Ser Val Leu Tyr Leu Leu Ile Gly Leu Arg Leu Arg Arg Glu Arg Leu
 225 230 235 240
 20 Leu Leu Met Gln Glu Ala Lys Gly Arg Gly Ser Ala Ala Ala Arg Ser
 245 250 255
 Arg Tyr Thr Cys Arg Leu Gln Gln His Asp Arg Gly Arg Arg Gln Val
 260 265 270
 Thr Lys Met Leu Phe Val Leu Val Val Val Phe Gly Ile Cys Trp Ala
 275 280 285
 25 Pro Phe His Ala Asp Arg Val Met Trp Ser Val Val Ser Gln Trp Thr
 290 295 300
 Asp Gly Leu His Leu Ala Phe Gln His Val His Val Ile Ser Gly Ile
 305 310 315 320
 30 Phe Phe Tyr Leu Gly Ser Ala Ala Asn Pro Val Leu Tyr Ser Leu Met
 325 330 335
 Ser Ser Arg Phe Arg Glu Thr Phe Gln Glu Ala Leu Cys Leu Gly Ala
 340 345 350
 Cys Cys His Arg Leu Arg Pro Arg His Ser Ser His Ser Leu Ser Arg
 355 360 365
 35 Met Thr Thr Gly Ser Thr Leu Cys Asp Val Gly Ser Leu Gly Ser Trp
 370 375 380
 Val His Pro Leu Ala Gly Asn Asp Gly Pro Glu Ala Gln Gln Glu Thr

385

390

395

400

Asp Pro Ser

(116) INFORMATION FOR SEQ ID NO:115:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 10 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GGAAGCTTCA GGCCCAAAGA TGGGGAACAT

30

(117) INFORMATION FOR SEQ ID NO:116:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GTGGATCCAC CCGCGGAGGA CCCAGGCTAG

30

(118) INFORMATION FOR SEQ ID NO:117:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1098 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

30 ATGGGGAACA TCACTGCAGA CAACTCCTCG ATGAGCTGTA CCATCGACCA TACCATCCAC 60
CAGACGCTGG CCCCGGTGGT CTATGTTACC GTGCTGGTGG TGGGCTTCCC GGCCAACTGC 120
CTGTCCCTCT ACTTCGGCTA CCTGCAGATC AAGGCCCGGA ACGAGCTGGG CGTGTACCTG 180
TGCAACCTGA CGGTGGCCGA CCTCTTCTAC ATCTGCTCGC TGCCCTTCTG GCTGCAGTAC 240
GTGCTGCAGC ACGACAACTG GTCTCACGGC GACCTGTCCT GCCAGGTGTG CGGCATCCTC 300
35 CTGTACGAGA ACATCTACAT CAGCGTGGGC TTCCTCTGCT GCATCTCCGT GGACCGCTAC 360

```

CTGGCTGTGG CCCATCCCTT CCGCTTCCAC CAGTTCCGGA CCCTGAAGGC GGCCGTGCGC 420
GTCAGCGTGG TCATCTGGGC CAAGGAGCTG CTGACCAGCA TCTACTTCCT GATGCACGAG 480
GAGGTCATCG AGGACGAGAA CCAGCACCGC GTGTGCTTTG AGCACTACCC CATCCAGGCA 540
TGGCAGCGCG CCATCAACTA CTACCGCTTC CTGGTGGGCT TCCTCTTCCC CATCTGCCTG 600
5 CTGCTGGCGT CCTACCAGGG CATCCTGCGC GCCGTGCGCC GGAGCCACGG CACCCAGAAG 660
AGCCGCAAGG ACCAGATCCA GCGGCTGGTG CTCAGCACCG TGGTCATCTT CCTGGCCTGC 720
TTCCTGCCCT ACCACGTGTT GCTGCTGGTG CGCAGCGTCT GGGAGGCCAG CTGCGACTTC 780
GCCAAGGGCG TTTTCAACGC CTACCACTTC TCCCTCCTGC TCACCAGCTT CAACTGCGTC 840
GCCGACCCCG TGCTCTACTG CTTCGTCAGC GAGACCACCC ACCGGGACCT GGCCCGCCTC 900
10 CGCGGGGCCT GCCTGGCCTT CCTCACCTGC TCCAGGACCG GCCGGGCCAG GGAGGCCTAC 960
CCGCTGGGTG CCCCCGAGGC CTCGGGAAA AGCGGGGCC AGGGTGAGGA GCCCGAGCTG 1020
TTGACCAAGC TCCACCCGGC CTTCCAGACC CCTAACTCGC CAGGGTCGGG CGGGTTCCCC 1080
ACGGGCAGGT TGGCCTAG 1098

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(119) INFORMATION FOR SEQ ID NO:118:

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15 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 365 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS:
    (D) TOPOLOGY: not relevant

20 (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Met Gly Asn Ile Thr Ala Asp Asn Ser Ser Met Ser Cys Thr Ile Asp
1          5          10          15

His Thr Ile His Gln Thr Leu Ala Pro Val Val Tyr Val Thr Val Leu
25          20          25          30

Val Val Gly Phe Pro Ala Asn Cys Leu Ser Leu Tyr Phe Gly Tyr Leu
35          40          45

Gln Ile Lys Ala Arg Asn Glu Leu Gly Val Tyr Leu Cys Asn Leu Thr
50          55          60

30 Val Ala Asp Leu Phe Tyr Ile Cys Ser Leu Pro Phe Trp Leu Gln Tyr
65          70          75          80

Val Leu Gln His Asp Asn Trp Ser His Gly Asp Leu Ser Cys Gln Val
85          90          95

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	Cys Gly Ile Leu Leu Tyr Glu Asn Ile Tyr Ile Ser Val Gly Phe Leu	
	100	105 110
	Cys Cys Ile Ser Val Asp Arg Tyr Leu Ala Val Ala His Pro Phe Arg	
	115	120 125
5	Phe His Gln Phe Arg Thr Leu Lys Ala Ala Val Gly Val Ser Val Val	
	130	135 140
	Ile Trp Ala Lys Glu Leu Leu Thr Ser Ile Tyr Phe Leu Met His Glu	
	145	150 155 160
10	Glu Val Ile Glu Asp Glu Asn Gln His Arg Val Cys Phe Glu His Tyr	
	165	170 175
	Pro Ile Gln Ala Trp Gln Arg Ala Ile Asn Tyr Tyr Arg Phe Leu Val	
	180	185 190
	Gly Phe Leu Phe Pro Ile Cys Leu Leu Leu Ala Ser Tyr Gln Gly Ile	
	195	200 205
15	Leu Arg Ala Val Arg Arg Ser His Gly Thr Gln Lys Ser Arg Lys Asp	
	210	215 220
	Gln Ile Gln Arg Leu Val Leu Ser Thr Val Val Ile Phe Leu Ala Cys	
	225	230 235 240
20	Phe Leu Pro Tyr His Val Leu Leu Leu Val Arg Ser Val Trp Glu Ala	
	245	250 255
	Ser Cys Asp Phe Ala Lys Gly Val Phe Asn Ala Tyr His Phe Ser Leu	
	260	265 270
	Leu Leu Thr Ser Phe Asn Cys Val Ala Asp Pro Val Leu Tyr Cys Phe	
	275	280 285
25	Val Ser Glu Thr Thr His Arg Asp Leu Ala Arg Leu Arg Gly Ala Cys	
	290	295 300
	Leu Ala Phe Leu Thr Cys Ser Arg Thr Gly Arg Ala Arg Glu Ala Tyr	
	305	310 315 320
30	Pro Leu Gly Ala Pro Glu Ala Ser Gly Lys Ser Gly Ala Gln Gly Glu	
	325	330 335
	Glu Pro Glu Leu Leu Thr Lys Leu His Pro Ala Phe Gln Thr Pro Asn	
	340	345 350
	Ser Pro Gly Ser Gly Gly Phe Pro Thr Gly Arg Leu Ala	
	355	360 365

35 (120) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

GACCTCGAGT CCTTCTACAC CTCATC

26

(121) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

15 TGCTCTAGAT TCCAGATAGG TGAAAACCTTG

30

(122) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 1416 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

ATGGATATTC TTTGTGAAGA AAATACTTCT TTGAGCTCAA CTACGAACTC CCTAATGCAA 60

25 TTAAATGATG ACAACAGGCT CTACAGTAAT GACTTTAACT CCGGAGAAGC TAACACTTCT 120

GATGCATTTA ACTGGACAGT CGACTCTGAA AATCGAACCA ACCTTTCCTG TGAAGGGTGC 180

CTCTCACCGT CGTGTCTCTC CTTACTTCAT CTCCAGGAAA AAAACTGGTC TGCTTTACTG 240

ACAGCCGTAG TGATTATTCT AACTATTGCT GGAAACATAC TCGTCATCAT GGCAGTGTCC 300

CTAGAGAAAA AGCTGCAGAA TGCCACCAAC TATTTCTGTA TGTCAGTTGC CATAGCTGAT 360

30 ATGCTGCTGG GTTTCCTTGT CATGCCCGTG TCCATGTTAA CCATCCTGTA TGGGTACCGG 420

TGGCCTCTGC CGAGCAAGCT TTGTGCAGTC TGGATTTACC TGGACGTGCT CTTCTCCACG 480

GCCTCCATCA TGCACCTCTG CGCCATCTCG CTGGACCGCT ACGTCGCCAT CCAGAATCCC 540

ATCCACCACA GCCGCTTCAA CTCCAGAACT AAGGCATTTT TGAAAATCAT TGCTGTTTGG 600

ACCATATCAG TAGGTATATC CATGCCAATA CCAGTCTTTG GGCTACAGGA CGATTCTGAAG 660
 GTCTTTAAGG AGGGGAGTTG CTTACTCGCC GATGATAACT TTGTCCTGAT CGGCTCTTTT 720
 GTGTCATTTT TCATTCCCTT AACCATCATG GTGATCACCT ACTTTCTAAC TATCAAGTCA 780
 CTCCAGAAAG AAGCTACTTT GTGTGFAAGT GATCTTGGCA CACGGGCCAA ATTAGCTTCT 840
 5 TTCAGCTTCC TCCCTCAGAG TTCTTTGTCT TCAGAAAAGC TCTTCCAGCG GTCGATCCAT 900
 AGGGAGCCAG GGTCTACAC AGGCAGGAGG ACTATGCAGT CCATCAGCAA TGAGCAAAAG 960
 GCATGCAAGG TGCTGGGCAT CGTCTTCTTC CTGTTTGTGG TGATGTGGTG CCCTTTCTTC 1020
 ATCACAAACA TCATGGCCGT CATCTGCAA GAGTCCTGCA ATGAGGATGT CATTGGGGCC 1080
 CTGCTCAATG TGTTTGTTTG GATCGGTTAT CTCTCTTCAG CAGTCAACCC ACTAGTCTAC 1140
 10 ACACTGTTCA ACAAGACCTA TAGGTCAGCC TTTTCACGGT ATATTCAGTG TCAGTACAAG 1200
 GAAAACAAAA AACCATTGCA GTTAATTTTA GTGAACACAA TACCGGCTTT GGCCTACAAG 1260
 TCTAGCCAAC TTCAAATGGG ACAAAAAAAG AATTCAAAGC AAGATGCCAA GACAACAGAT 1320
 AATGACTGCT CAATGGTTGC TCTAGGAAAG CAGTATTCTG AAGAGGCTTC TAAAGACAAT 1380
 AGCGACGGAG TGAATGAAAA GGTGAGCTGT GTGTGA 1416

15 (123) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 471 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - 20 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Met Asp Ile Leu Cys Glu Glu Asn Thr Ser Leu Ser Ser Thr Thr Asn
 1 5 10 15
 25 Ser Leu Met Gln Leu Asn Asp Asp Asn Arg Leu Tyr Ser Asn Asp Phe
 20 25 30
 Asn Ser Gly Glu Ala Asn Thr Ser Asp Ala Phe Asn Trp Thr Val Asp
 35 40 45
 30 Ser Glu Asn Arg Thr Asn Leu Ser Cys Glu Gly Cys Leu Ser Pro Ser
 50 55 60
 Cys Leu Ser Leu Leu His Leu Gln Glu Lys Asn Trp Ser Ala Leu Leu
 65 70 75 80

	Thr	Ala	Val	Val	Ile	Ile	Leu	Thr	Ile	Ala	Gly	Asn	Ile	Leu	Val	Ile	
					85					90					95		
	Met	Ala	Val	Ser	Leu	Glu	Lys	Lys	Leu	Gln	Asn	Ala	Thr	Asn	Tyr	Phe	
				100					105					110			
5	Leu	Met	Ser	Leu	Ala	Ile	Ala	Asp	Met	Leu	Leu	Gly	Phe	Leu	Val	Met	
				115				120					125				
	Pro	Val	Ser	Met	Leu	Thr	Ile	Leu	Tyr	Gly	Tyr	Arg	Trp	Pro	Leu	Pro	
				130			135					140					
10	Ser	Lys	Leu	Cys	Ala	Val	Trp	Ile	Tyr	Leu	Asp	Val	Leu	Phe	Ser	Thr	
	145					150					155					160	
	Ala	Ser	Ile	Met	His	Leu	Cys	Ala	Ile	Ser	Leu	Asp	Arg	Tyr	Val	Ala	
				165						170					175		
	Ile	Gln	Asn	Pro	Ile	His	His	Ser	Arg	Phe	Asn	Ser	Arg	Thr	Lys	Ala	
				180					185					190			
15	Phe	Leu	Lys	Ile	Ile	Ala	Val	Trp	Thr	Ile	Ser	Val	Gly	Ile	Ser	Met	
			195					200					205				
	Pro	Ile	Pro	Val	Phe	Gly	Leu	Gln	Asp	Asp	Ser	Lys	Val	Phe	Lys	Glu	
		210					215					220					
20	Gly	Ser	Cys	Leu	Leu	Ala	Asp	Asp	Asn	Phe	Val	Leu	Ile	Gly	Ser	Phe	
	225					230					235					240	
	Val	Ser	Phe	Phe	Ile	Pro	Leu	Thr	Ile	Met	Val	Ile	Thr	Tyr	Phe	Leu	
				245						250					255		
	Thr	Ile	Lys	Ser	Leu	Gln	Lys	Glu	Ala	Thr	Leu	Cys	Val	Ser	Asp	Leu	
				260					265						270		
25	Gly	Thr	Arg	Ala	Lys	Leu	Ala	Ser	Phe	Ser	Phe	Leu	Pro	Gln	Ser	Ser	
			275					280					285				
	Leu	Ser	Ser	Glu	Lys	Leu	Phe	Gln	Arg	Ser	Ile	His	Arg	Glu	Pro	Gly	
		290					295					300					
30	Ser	Tyr	Thr	Gly	Arg	Arg	Thr	Met	Gln	Ser	Ile	Ser	Asn	Glu	Gln	Lys	
	305					310					315					320	
	Ala	Cys	Lys	Val	Leu	Gly	Ile	Val	Phe	Phe	Leu	Phe	Val	Val	Met	Trp	
					325					330					335		
	Cys	Pro	Phe	Phe	Ile	Thr	Asn	Ile	Met	Ala	Val	Ile	Cys	Lys	Glu	Ser	
				340					345					350			
35	Cys	Asn	Glu	Asp	Val	Ile	Gly	Ala	Leu	Leu	Asn	Val	Phe	Val	Trp	Ile	
		355						360					365				
	Gly	Tyr	Leu	Ser	Ser	Ala	Val	Asn	Pro	Leu	Val	Tyr	Thr	Leu	Phe	Asn	

97

370 375 380
 Lys Thr Tyr Arg Ser Ala Phe Ser Arg Tyr Ile Gln Cys Gln Tyr Lys
 385 390 395 400
 5 Glu Asn Lys Lys Pro Leu Gln Leu Ile Leu Val Asn Thr Ile Pro Ala
 405 410 415
 Leu Ala Tyr Lys Ser Ser Gln Leu Gln Met Gly Gln Lys Lys Asn Ser
 420 425 430
 Lys Gln Asp Ala Lys Thr Thr Asp Asn Asp Cys Ser Met Val Ala Leu
 435 440 445
 10 Gly Lys Gln Tyr Ser Glu Glu Ala Ser Lys Asp Asn Ser Asp Gly Val
 450 455 460
 Asn Glu Lys Val Ser Cys Val
 465 470

(124) INFORMATION FOR SEQ ID NO:123:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- 20 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

GACCTCGAGG TTGCTTAAGA CTGAAGC

27

(125) INFORMATION FOR SEQ ID NO:124:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

ATTCTAGAC ATATGTAGCT TGTACCG

27

(126) INFORMATION FOR SEQ ID NO:125:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1377 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

	ATGGTGAACC	TGAGGAATGC	GGTGCATTCA	TTCCTTGTGC	ACCTAATTGG	CCTATTGGTT	60
	TGGCAATGTG	ATATTTCTGT	GAGCCCAGTA	GCAGCTATAG	TAAGTGACAT	TTTCAATACC	120
5	TCCGATGGTG	GACGCTTCAA	ATTCCCAGAC	GGGGTACAAA	ACTGGCCAGC	ACTTTCAATC	180
	GTCATCATAA	TAATCATGAC	AATAGGTGGC	AACATCCTTG	TGATCATGGC	AGTAAGCATG	240
	GAAAAGAAAC	TGCACAATGC	CACCAATTAC	TTCTTAATGT	CCCTAGCCAT	TGCTGATATG	300
	CTAGTGGGAC	TACTTGTCAT	GCCCCGTGCT	CTCCTGGCAA	TCCTTTATGA	TTATGTCTGG	360
	CCACTACCTA	GATATTTGTG	CCCCGTCTGG	ATTTCTTTAG	ATGTTTTATT	TTCAACAGCG	420
10	TCCATCATGC	ACCTCTGCGC	TATATCGCTG	GATCGGTATG	TAGCAATACG	TAATCCTATT	480
	GAGCATAGCC	GTTTCAATTC	GCGGACTAAG	GCCATCATGA	AGATTGCTAT	TGTTTGGGCA	540
	ATTTCTATAG	GTGTATCAGT	TCCTATCCCT	GTGATTGGAC	TGAGGGACGA	AGAAAAGGTG	600
	TTCGTGAACA	ACACGACGTG	CGTGCTCAAC	GACCCAAATT	TCGTTCTTAT	TGGGTCCTTC	660
	GTAGCTTTCT	TCATACCGCT	GACGATTATG	GTGATTACGT	ATTGCCTGAC	CATCTACGTT	720
15	CTGCGCCGAC	AAGCTTTGAT	GTTACTGCAC	GGCCACACCG	AGGAACCGCC	TGGACTAAGT	780
	CTGGATTTCC	TGAAGTGCTG	CAAGAGGAAT	ACGGCCGAGG	AAGAGAACTC	TGCAAACCCT	840
	AACCAAGACC	AGAACGCACG	CCGAAGAAAG	AAGAAGGAGA	GACGTCCTAG	GGGCACCATG	900
	CAGGCTATCA	ACAATGAAAG	AAAAGCTTCG	AAAGTCCTTG	GGATTGTTTT	CTTTGTGFTT	960
	CTGATCATGT	GGTGCCCAT	TTTCATTACC	AATATTCTGT	CTGTTCTTTG	TGAGAAGTCC	1020
20	TGTAACCAAA	AGCTCATGGA	AAAGCTTCTG	AATGTGTTTG	TTTGGATTGG	CTATGTTTGT	1080
	TCAGGAATCA	ATCCTCTGGT	GTATACTCTG	TTCAACAAAA	TTTACCGAAG	GGCATTCTCC	1140
	AACTATTTGC	GTTGCAATTA	TAAGGTAGAG	AAAAAGCCTC	CTGTCAGGCA	GATTCCAAGA	1200
	GTTGCCGCCA	CTGCTTTGTC	TGGGAGGGAG	CTTAATGTTA	ACATTTATCG	GCATACCAAT	1260
	GAACCGGTGA	TCGAGAAAGC	CAGTGACAA	TAGAGATGCA	AGTTGAGAAT		1320
25	TTAGAGTTAC	CAGTAAATCC	CTCCAGTGTG	GTTAGCGAAA	GGATTAGCAG	TGTGTGA	1377

(127) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 458 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

```

5  Met Val Asn Leu Arg Asn Ala Val His Ser Phe Leu Val His Leu Ile
   1           5           10           15

   Gly Leu Leu Val Trp Gln Cys Asp Ile Ser Val Ser Pro Val Ala Ala
   20           25           30

10  Ile Val Thr Asp Ile Phe Asn Thr Ser Asp Gly Gly Arg Phe Lys Phe
   35           40           45

   Pro Asp Gly Val Gln Asn Trp Pro Ala Leu Ser Ile Val Ile Ile Ile
   50           55           60

   Ile Met Thr Ile Gly Gly Asn Ile Leu Val Ile Met Ala Val Ser Met
   65           70           75           80

15  Glu Lys Lys Leu His Asn Ala Thr Asn Tyr Phe Leu Met Ser Leu Ala
   85           90           95

   Ile Ala Asp Met Leu Val Gly Leu Leu Val Met Pro Leu Ser Leu Leu
   100          105          110

   Ala Ile Leu Tyr Asp Tyr Val Trp Pro Leu Pro Arg Tyr Leu Cys Pro
   115          120          125

20  Val Trp Ile Ser Leu Asp Val Leu Phe Ser Thr Ala Ser Ile Met His
   130          135          140

   Leu Cys Ala Ile Ser Leu Asp Arg Tyr Val Ala Ile Arg Asn Pro Ile
   145          150          155          160

25  Glu His Ser Arg Phe Asn Ser Arg Thr Lys Ala Ile Met Lys Ile Ala
   165          170          175

   Ile Val Trp Ala Ile Ser Ile Gly Val Ser Val Pro Ile Pro Val Ile
   180          185          190

   Gly Leu Arg Asp Glu Glu Lys Val Phe Val Asn Asn Thr Thr Cys Val
   195          200          205

30  Leu Asn Asp Pro Asn Phe Val Leu Ile Gly Ser Phe Val Ala Phe Phe
   210          215          220

   Ile Pro Leu Thr Ile Met Val Ile Thr Tyr Cys Leu Thr Ile Tyr Val
   225          230          235          240

35  Leu Arg Arg Gln Ala Leu Met Leu Leu His Gly His Thr Glu Glu Pro
   245          250          255

```

100

Pro Gly Leu Ser Leu Asp Phe Leu Lys Cys Cys Lys Arg Asn Thr Ala
 260 265 270
 Glu Glu Glu Asn Ser Ala Asn Pro Asn Gln Asp Gln Asn Ala Arg Arg
 275 280 285
 5 Arg Lys Lys Lys Glu Arg Arg Pro Arg Gly Thr Met Gln Ala Ile Asn
 290 295 300
 Asn Glu Arg Lys Ala Ser Lys Val Leu Gly Ile Val Phe Phe Val Phe
 305 310 315 320
 10 Leu Ile Met Trp Cys Pro Phe Phe Ile Thr Asn Ile Leu Ser Val Leu
 325 330 335
 Cys Glu Lys Ser Cys Asn Gln Lys Leu Met Glu Lys Leu Leu Asn Val
 340 345 350
 Phe Val Trp Ile Gly Tyr Val Cys Ser Gly Ile Asn Pro Leu Val Tyr
 355 360 365
 15 Thr Leu Phe Asn Lys Ile Tyr Arg Arg Ala Phe Ser Asn Tyr Leu Arg
 370 375 380
 Cys Asn Tyr Lys Val Glu Lys Lys Pro Pro Val Arg Gln Ile Pro Arg
 385 390 395 400
 20 Val Ala Ala Thr Ala Leu Ser Gly Arg Glu Leu Asn Val Asn Ile Tyr
 405 410 415
 Arg His Thr Asn Glu Pro Val Ile Glu Lys Ala Ser Asp Asn Glu Pro
 420 425 430
 Gly Ile Glu Met Gln Val Glu Asn Leu Glu Leu Pro Val Asn Pro Ser
 435 440 445
 25 Ser Val Val Ser Glu Arg Ile Ser Ser Val
 450 455

(128) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 30 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

35 GGTAAGCTTG GCAGTCCACG CCAGGCCTTC

30

(129) INFORMATION FOR SEQ ID NO:128:

101

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
5 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

TCCGAATTCT CTGTAGACAC AAGGCTTTGG

30

(130) INFORMATION FOR SEQ ID NO:129:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1068 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- 15 (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

ATGGATCAGT	TCCCTGAATC	AGTGACAGAA	AACTTTGAGT	ACGATGATTT	GGCTGAGGCC	60
TGTTATATTG	GGGACATCGT	GGTCTTTGGG	ACTGTGTTCC	TGTCCATATT	CTACTCCGTC	120
ATCTTTGCCA	TTGGCCTGGT	GGGAAATTTG	TTGGTAGTGT	TTGCCCTCAC	CAACAGCAAG	180
20 AAGCCCAAGA	GTGTCACCGA	CATTTACCTC	CTGAACCTGG	CCTGTCTGA	TCTGCTGTTT	240
GTAGCCACTT	TGCCCTTCTG	GACTCACTAT	TTGATAAATG	AAAAGGGCCT	CCACAATGCC	300
ATGTGCAAAT	TCACTACCGC	CTTCTTCTTC	ATCGGCTTTT	TTGGAAGCAT	ATTCTTCATC	360
ACCGTCATCA	GCATTGATAG	GTACCTGGCC	ATCGTCCTGG	CCGCCAACTC	CATGAACAAC	420
CGGACCGTGC	AGCATGGCGT	CACCATCAGC	CTAGGCGTCT	GGGCAGCAGC	CATTTTGGTG	480
25 GCAGCACCCC	AGTTCATGTT	CACAAAGCAG	AAAGAAAATG	AATGCCTTGG	TGACTACCCC	540
GAGGTCCTCC	AGGAAATCTG	GCCCCTGCTC	CGCAATGTGG	AAACAAATTT	TCTTGGCTTC	600
CTACTCCCCC	TGCTCAATTAT	GAGTTATTGC	TACTTCAGAA	TCATCCAGAC	GCTGTTTTC	660
TGCAAGAACC	ACAAGAAAGC	CAAAGCCATT	AAACTGATCC	TTCTGGTGGT	CATCGTGTTT	720
TTCTCTTCT	GGACACCCTA	CAACGTTATG	ATTTTCCTGG	AGACGCTTAA	GCTCTATGAC	780
30 TTCTTTCCCA	GTTGTGACAT	GAGGAAGGAT	CTGAGGCTGG	CCCTCAGTGT	GA CTGAGACG	840
GTTGCATTTA	GCCATTGTTG	CCTGAATCCT	CTCATCTATG	CATTTGCTGG	GGAGAAGTTC	900
AGAAGATACC	TTTACCACCT	GTATGGGAAA	TGCCTGGCTG	TCCTGTGTGG	GCGCTCAGTC	960

CACGTTGATT TCTCCTCATC TGAATCACAA AGGAGCAGGC ATGGAAGTGT TCTGAGCAGC 1020

AATTTTACTT ACCACACGAG TGATGGAGAT GCATTGCTCC TTCTCTGA 1068

(131) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 355 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Met	Asp	Gln	Phe	Pro	Glu	Ser	Val	Thr	Glu	Asn	Phe	Glu	Tyr	Asp	Asp	1	5	10	15
Leu	Ala	Glu	Ala	Cys	Tyr	Ile	Gly	Asp	Ile	Val	Val	Phe	Gly	Thr	Val	20	25	30	
Phe	Leu	Ser	Ile	Phe	Tyr	Ser	Val	Ile	Phe	Ala	Ile	Gly	Leu	Val	Gly	35	40	45	
Asn	Leu	Leu	Val	Val	Phe	Ala	Leu	Thr	Asn	Ser	Lys	Lys	Pro	Lys	Ser	50	55	60	
Val	Thr	Asp	Ile	Tyr	Leu	Leu	Asn	Leu	Ala	Leu	Ser	Asp	Leu	Leu	Phe	65	70	75	80
Val	Ala	Thr	Leu	Pro	Phe	Trp	Thr	His	Tyr	Leu	Ile	Asn	Glu	Lys	Gly	85	90	95	
Leu	His	Asn	Ala	Met	Cys	Lys	Phe	Thr	Thr	Ala	Phe	Phe	Phe	Ile	Gly	100	105	110	
Phe	Phe	Gly	Ser	Ile	Phe	Phe	Ile	Thr	Val	Ile	Ser	Ile	Asp	Arg	Tyr	115	120	125	
Leu	Ala	Ile	Val	Leu	Ala	Ala	Asn	Ser	Met	Asn	Asn	Arg	Thr	Val	Gln	130	135	140	
His	Gly	Val	Thr	Ile	Ser	Leu	Gly	Val	Trp	Ala	Ala	Ala	Ile	Leu	Val	145	150	155	160
Ala	Ala	Pro	Gln	Phe	Met	Phe	Thr	Lys	Gln	Lys	Glu	Asn	Glu	Cys	Leu	165	170	175	
Gly	Asp	Tyr	Pro	Glu	Val	Leu	Gln	Glu	Ile	Trp	Pro	Val	Leu	Arg	Asn	180	185	190	
Val	Glu	Thr	Asn	Phe	Leu	Gly	Phe	Leu	Leu	Pro	Leu	Leu	Ile	Met	Ser	195	200	205	

103

Tyr Cys Tyr Phe Arg Ile Ile Gln Thr Leu Phe Ser Cys Lys Asn His
 210 215 220
 Lys Lys Ala Lys Ala Ile Lys Leu Ile Leu Leu Val Val Ile Val Phe
 225 230 235 240
 5 Phe Leu Phe Trp Thr Pro Tyr Asn Val Met Ile Phe Leu Glu Thr Leu
 245 250 255
 Lys Leu Tyr Asp Phe Phe Pro Ser Cys Asp Met Arg Lys Asp Leu Arg
 260 265 270
 10 Leu Ala Leu Ser Val Thr Glu Thr Val Ala Phe Ser His Cys Cys Leu
 275 280 285
 Asn Pro Leu Ile Tyr Ala Phe Ala Gly Glu Lys Phe Arg Arg Tyr Leu
 290 295 300
 Tyr His Leu Tyr Gly Lys Cys Leu Ala Val Leu Cys Gly Arg Ser Val
 305 310 315 320
 15 His Val Asp Phe Ser Ser Ser Glu Ser Gln Arg Ser Arg His Gly Ser
 325 330 335
 Val Leu Ser Ser Asn Phe Thr Tyr His Thr Ser Asp Gly Asp Ala Leu
 340 345 350
 20 Leu Leu Leu
 355

(132) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

GATCTCCAGT AGGCATAAGT GGACAATTCT GG

32

30 (133) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

CTCCTTCGGT CCTCCTATCG TTGTCAGAAG

30

(134) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

10 AGAAGGCCAA GATCGCGCGG CTGGCCCTCA

30

(135) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

CGGCGCCACC GCACGAAAAA GCTCATCTTC

30

20 (136) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

GCCAAGAAGC GGGTGAAGTT CCTGGTGGTG GCA

33

(137) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

CAGGCGGAAG GTGAAAGTCC TGGTCCTCGT

30

(138) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

CGGCGCCTGC GGGCCAAGCG GCTGGTGGTG GTG

33

(139) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

20 CCAAGCACAA AGCCAAGAAA GTGACCATCA C

31

(140) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GCGCCGGCGC ACCAAATGCT TGCTGGTGGT

30

30 (141) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

106

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

CAAAAAGCTG AAGAAATCTA AGAAGATCAT CTTTATTGTC G

41

(142) INFORMATION FOR SEQ ID NO:141:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

CAAGACCAAG GCAAAACGCA TGATCGCCAT

30

(143) INFORMATION FOR SEQ ID NO:142:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

GTCAAGGAGA AGTCCAAAAG GATCATCATC

30

(144) INFORMATION FOR SEQ ID NO:143:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

30

CGCCGCGTGC GGGCCAAGCA GCTCCTGCTC

30

(145) INFORMATION FOR SEQ ID NO:144:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

107

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

CCTGATAAGC GCTATAAAAT GGTCTGTGTTT CGA

33

(146) INFORMATION FOR SEQ ID NO:145:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

GAAAGACAAA AGAGAGTCAA GAGGATGTCT TTATTG

36

(147) INFORMATION FOR SEQ ID NO:146:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

CGGAGAAAGA GGGTGAAACG CACAGCCATC GCC

33

(148) INFORMATION FOR SEQ ID NO:147:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

30 AAGCTTCAGC GGGCCAAGGC ACTGGTCACC

30

(149) INFORMATION FOR SEQ ID NO:148:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

108

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

CAGCGGCAGA AGGC¹AAAAG GGTGGCCATC

30

(150) INFORMATION FOR SEQ ID NO:149:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

CGGCAGAAGG CGAAGCGCAT GATCCTCGCG

30

(151) INFORMATION FOR SEQ ID NO:150:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

GAGCGCAACA AGGCCAAAAA GGTGATCATC

30

(152) INFORMATION FOR SEQ ID NO:151:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

30 GGTGTAAACA AAAAGGCTAA AACACAATT ATTCTTATT

39

(153) INFORMATION FOR SEQ ID NO:152:

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

109

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

GAGAGCCAGC TCAAGAGCAC CGTGGTG

27

(154) INFORMATION FOR SEQ ID NO:153:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

CCACAAGCAA ACCAAGAAAA TGCTGGCTGT

30

(155) INFORMATION FOR SEQ ID NO:154:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

CATCAAGTGT ATCATGTGCC AAGTAGCCCC

30

(156) INFORMATION FOR SEQ ID NO:155:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

30 CTAGAGAGTC AGATGAAGTG TACAGTAGTG GCAC

34

(157) INFORMATION FOR SEQ ID NO:156:

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

110

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

CGGACAAAAG TGAAAATAA AAAGATGTTC CTCATT

36

(158) INFORMATION FOR SEQ ID NO:157:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

GCTGAGGTTC GCAATAAACT AACCATGTTT GTG

33

(159) INFORMATION FOR SEQ ID NO:158:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

GGGAGGCCGA GCTGAAAGCC ACCCTGCTC

29

(160) INFORMATION FOR SEQ ID NO:159:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

30 CAAGATCAAG AGAGCCAAAA CCTTCATCAT G

31

(161) INFORMATION FOR SEQ ID NO:160:

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

CCGGAGACAA GTGAAGAAGA TGCTGTTTGT C

31

(162) INFORMATION FOR SEQ ID NO:161:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

GCAAGGACCA GATCAAGCGG CTGGTGCTCA

30

(163) INFORMATION FOR SEQ ID NO:162:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

CAAGAAAGCC AAAGCCAAGA AACTGATCCT TCTG

34

(164) INFORMATION FOR SEQ ID NO:163:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1068 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

30 ATGGAAGATT TGGAGGAAAC ATTATTTGAA GAATTTGAAA ACTATTCCTA TGACCTAGAC 60
TATTACTCTC TGGAGTCTGA TTTGGAGGAG AAAGTCCAGC TGGGAGTTGT TCACTGGGTC 120
TCCCTGGTGT TATATTGTTT GGCTTTTGTT CTGGGAATTC CAGGAAATGC CATCGTCATT 180
TGGTTACGGG GGCTCAAGTG GAAGAAGACA GTCACCACTC TGTGGTTCCT CAATCTAGCC 240
ATTGCGGATT TCATTTTCT TCTCTTCTG CCCCTGTACA TCTCCTATGT GGCCATGAAT 300

TTCCACTGGC CCTTTGGCAT CTGGCTGTGC AAAGCCAATT CCTTCACTGC CCAGTTGAAC 360
 ATGTTTGCCA GTGTTTTTTT CCTGACAGTG ATCAGCCTGG ACCACTATAT CCACTTGATC 420
 CATCCTGTCT TATCTCATCG GCATCGAACC CTCAAGAACT CTCTGATTGT CATTATATTC 480
 ATCTGGCTTT TGGCTTCTCT AATTGGCGGT CCTGCCCTGT ACTTCCGGGA CACTGTGGAG 540
 5 TTCAATAATC ATACTCTTTG CTATAACAAT TTTCAGAAGC ATGATCCTGA CCTCACTTTG 600
 ATCAGGCACC ATGTTCTGAC TTGGGTGAAA TTTATCATTG GCTATCTCTT CCCTTTGCTA 660
 ACAATGAGTA TTTGCTACTT GTGTCTCATC TTCAAGGTGA AGAAGCGAAC AGTCCTGATC 720
 TCCAGTAGGC ATAAGTGGAC AATTCTGGTT GTGGTTGTGG CCTTTGTGGT TTGCTGGACT 780
 CCTTATCACC TGTTTAGCAT TTGGGAGCTC ACCATTACACC ACAATAGCTA TTCCCACCAT 840
 10 GTGATGCAGG CTGGAATCCC CCTCTCCACT GGTTCGGCAT TCCTCAATAG TTGCTTGAAC 900
 CCCATCCTTT ATGTCCTAAT TAGTAAGAAG TTCCAAGCTC GCTTCCGGTC CTCAGTTGCT 960
 GAGATACTCA AGTACACACT GTGGGAAGTC AGCTGTTCTG GCACAGTGAG TGAACAGCTC 1020
 AGGAACTCAG AAACCAAGAA TCTGTGTCTC CTGGAAACAG CTCAATAA 1068

(165) INFORMATION FOR SEQ ID NO:164:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 355 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant
- 20 (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Met Glu Asp Leu Glu Glu Thr Leu Phe Glu Glu Phe Glu Asn Tyr Ser
 1 5 10 15
 Tyr Asp Leu Asp Tyr Tyr Ser Leu Glu Ser Asp Leu Glu Glu Lys Val
 20 25 30
 Gln Leu Gly Val Val His Trp Val Ser Leu Val Leu Tyr Cys Leu Ala
 35 40 45
 Phe Val Leu Gly Ile Pro Gly Asn Ala Ile Val Ile Trp Phe Thr Gly
 50 55 60
 30 Leu Lys Trp Lys Lys Thr Val Thr Thr Leu Trp Phe Leu Asn Leu Ala
 65 70 75 80
 Ile Ala Asp Phe Ile Phe Leu Leu Phe Leu Pro Leu Tyr Ile Ser Tyr
 85 90 95

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Val Ala Met Asn Phe His Trp Pro Phe Gly Ile Trp Leu Cys Lys Ala
 100 105 110
 Asn Ser Phe Thr Ala Gln Leu Asn Met Phe Ala Ser Val Phe Phe Leu
 115 120 125
 5 Thr Val Ile Ser Leu Asp His Tyr Ile His Leu Ile His Pro Val Leu
 130 135 140
 Ser His Arg His Arg Thr Leu Lys Asn Ser Leu Ile Val Ile Ile Phe
 145 150 155 160
 10 Ile Trp Leu Leu Ala Ser Leu Ile Gly Gly Pro Ala Leu Tyr Phe Arg
 165 170 175
 Asp Thr Val Glu Phe Asn Asn His Thr Leu Cys Tyr Asn Asn Phe Gln
 180 185 190
 Lys His Asp Pro Asp Leu Thr Leu Ile Arg His His Val Leu Thr Trp
 195 200 205
 15 Val Lys Phe Ile Ile Gly Tyr Leu Phe Pro Leu Leu Thr Met Ser Ile
 210 215 220
 Cys Tyr Leu Cys Leu Ile Phe Lys Val Lys Lys Arg Thr Val Leu Ile
 225 230 235 240
 20 Ser Ser Arg His Lys Trp Thr Ile Leu Val Val Val Val Ala Phe Val
 245 250 255
 Val Cys Trp Thr Pro Tyr His Leu Phe Ser Ile Trp Glu Leu Thr Ile
 260 265 270
 His His Asn Ser Tyr Ser His His Val Met Gln Ala Gly Ile Pro Leu
 275 280 285
 25 Ser Thr Gly Leu Ala Phe Leu Asn Ser Cys Leu Asn Pro Ile Leu Tyr
 290 295 300
 Val Leu Ile Ser Lys Lys Phe Gln Ala Arg Phe Arg Ser Ser Val Ala
 305 310 315 320
 30 Glu Ile Leu Lys Tyr Thr Leu Trp Glu Val Ser Cys Ser Gly Thr Val
 325 330 335
 Ser Glu Gln Leu Arg Asn Ser Glu Thr Lys Asn Leu Cys Leu Leu Glu
 340 345 350
 Thr Ala Gln
 355

35 (166) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1089 base pairs

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(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

ATGGGCAACC ACACGTGGGA GGGCTGCCAC GTGGACTCGC GCGTGGACCA CCTCTTTCCG 60
CCATCCCTCT ACATCTTTGT CATCGGCGTG GGGCTGCCCA CCAACTGCCT GGCTCTGTGG 120
GCGGCCTACC GCCAGGTGCA ACAGCGCAAC GAGCTGGGCG TCTACCTGAT GAACCTCAGC 180
ATCGCCGACC TGCTGTACAT CTGCACGCTG CCGCTGTGGG TGGACTACTT CCTGCACCAC 240
10 GACAACTGGA TCCACGGCCC CGGGTCTGTC AAGCTCTTTG GGTTCATCTT CTACACCAAT 300
ATCTACATCA GCATCGCCTT CCTGTGCTGC ATCTCGGTGG ACCGCTACCT GGCTGTGGCC 360
CACCCACTCC GCTTCGCCCC CCTGCGCCCG GTCAAGACCG CCGTGGCCGT GAGCTCCGTG 420
GTCTGGGCCA CGGAGCTGGG CGCCAACTCG GCGCCCCTGT TCCATGACGA GCTCTTCCGA 480
GACCGCTACA ACCACACCTT CTGCTTTGAG AAGTTCCCCA TGGAAGGCTG GGTGGCCTGG 540
15 ATGAACCTCT ATCGGGTGTT CGTGGGCTTC CTCTTCCCGT GGGCGCTCAT GCTGCTGTCTG 600
TACCGGGGCA TCCTGCGGGC CGTGCGGGGC AGCGTGTCCA CCGAGCGCCA GGAGAAGGCC 660
AAGATCGCGC GGCTGGCCCT CAGCCTCATC GCCATCGTGC TGGTCTGCTT TGCGCCCTAT 720
CACGTGCTCT TGCTGTCCCG CAGCGCCATC TACCTGGGCC GCCCTGGGA CTGCGGCTTC 780
GAGGAGCGCG TCTTTTCTGC ATACCACAGC TCACTGGCTT TCACCAGCCT GAACTGTGTG 840
20 GCGGACCCCA TCCTCTACTG CCTGGTCAAC GAGGGCGCCC GCAGCGATGT GGCCAAGGCC 900
CTGCACAACC TGCTCCGCTT TCTGGCCAGC GACAAGCCCC AGGAGATGGC CAATGCCTCG 960
CTCACCTGG AGACCCCACT CACCTCCAAG AGGAACAGCA CAGCCAAAGC CATGACTGGC 1020
AGCTGGGCGG CCACTCCGCC TTCCCAGGGG GACCAGGTGC AGCTGAAGAT GCTGCCGCCA 1080
GCACAATGA 1089

25 (167) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 362 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
30 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

	Met	Gly	Asn	His	Thr	Trp	Glu	Gly	Cys	His	Val	Asp	Ser	Arg	Val	Asp	
	1				5					10					15		
5	His	Leu	Phe	Pro	Pro	Ser	Leu	Tyr	Ile	Phe	Val	Ile	Gly	Val	Gly	Leu	
				20					25					30			
	Pro	Thr	Asn	Cys	Leu	Ala	Leu	Trp	Ala	Ala	Tyr	Arg	Gln	Val	Gln	Gln	
			35					40					45				
	Arg	Asn	Glu	Leu	Gly	Val	Tyr	Leu	Met	Asn	Leu	Ser	Ile	Ala	Asp	Leu	
			50				55					60					
10	Leu	Tyr	Ile	Cys	Thr	Leu	Pro	Leu	Trp	Val	Asp	Tyr	Phe	Leu	His	His	
	65					70					75				80		
	Asp	Asn	Trp	Ile	His	Gly	Pro	Gly	Ser	Cys	Lys	Leu	Phe	Gly	Phe	Ile	
					85					90					95		
15	Phe	Tyr	Thr	Asn	Ile	Tyr	Ile	Ser	Ile	Ala	Phe	Leu	Cys	Cys	Ile	Ser	
				100					105					110			
	Val	Asp	Arg	Tyr	Leu	Ala	Val	Ala	His	Pro	Leu	Arg	Phe	Ala	Arg	Leu	
			115					120					125				
	Arg	Arg	Val	Lys	Thr	Ala	Val	Ala	Val	Ser	Ser	Val	Val	Trp	Ala	Thr	
			130				135					140					
20	Glu	Leu	Gly	Ala	Asn	Ser	Ala	Pro	Leu	Phe	His	Asp	Glu	Leu	Phe	Arg	
	145					150					155					160	
	Asp	Arg	Tyr	Asn	His	Thr	Phe	Cys	Phe	Glu	Lys	Phe	Pro	Met	Glu	Gly	
				165						170					175		
25	Trp	Val	Ala	Trp	Met	Asn	Leu	Tyr	Arg	Val	Phe	Val	Gly	Phe	Leu	Phe	
			180						185					190			
	Pro	Trp	Ala	Leu	Met	Leu	Leu	Ser	Tyr	Arg	Gly	Ile	Leu	Arg	Ala	Val	
			195					200					205				
	Arg	Gly	Ser	Val	Ser	Thr	Glu	Arg	Gln	Glu	Lys	Ala	Lys	Ile	Ala	Arg	
		210					215					220					
30	Leu	Ala	Leu	Ser	Leu	Ile	Ala	Ile	Val	Leu	Val	Cys	Phe	Ala	Pro	Tyr	
	225					230					235				240		
	His	Val	Leu	Leu	Leu	Ser	Arg	Ser	Ala	Ile	Tyr	Leu	Gly	Arg	Pro	Trp	
				245						250				255			
35	Asp	Cys	Gly	Phe	Glu	Glu	Arg	Val	Phe	Ser	Ala	Tyr	His	Ser	Ser	Leu	
			260						265					270			
	Ala	Phe	Thr	Ser	Leu	Asn	Cys	Val	Ala	Asp	Pro	Ile	Leu	Tyr	Cys	Leu	

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275 280 285

Val Asn Glu Gly Ala Arg Ser Asp Val Ala Lys Ala Leu His Asn Leu
290 295 300

5 Leu Arg Phe Leu Ala Ser Asp Lys Pro Gln Glu Met Ala Asn Ala Ser
305 310 315 320

Leu Thr Leu Glu Thr Pro Leu Thr Ser Lys Arg Asn Ser Thr Ala Lys
325 330 335

Ala Met Thr Gly Ser Trp Ala Ala Thr Pro Pro Ser Gln Gly Asp Gln
340 345 350

10 Val Gln Leu Lys Met Leu Pro Pro Ala Gln
355 360

(168) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1002 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

20 ATGGAGTCCT CAGGCAACCC AGAGAGCACC ACCTTTTTTT ACTATGACCT TCAGAGCCAG 60
 CCGTGTGAGA ACCAGGCCTG GGTCTTTGCT ACCCTCGCCA CCACTGTCCT GTACTGCCTG 120
 GTGTTTCTCC TCAGCCTAGT GGGCAACAGC CTGGTCCTGT GGGTCCTGGT GAAGTATGAG 180
 AGCCTGGAGT CCCTCACCAA CATCTTCATC CTCAACCTGT GCCTCTCAGA CCTGGTGTTC 240
 GCCTGCTTGT TGCTGTGTG GATCTCCCCA TACCACTGGG GCTGGGTGCT GGGAGACTTC 300

25 CTCTGCAAAC TCCTCAATAT GATCTTCTCC ATCAGCCTCT ACAGCAGCAT CTTCTTCTG 360
 ACCATCATGA CCATCCACCG CTACCTGTG GTAGTGAGCC CCCTCTCCAC CCTGCGCGTC 420
 CCCACCCTCC GCTGCCGGGT GCTGGTGACC ATGGCTGTGT GGGTAGCCAG CATCCTGTCC 480
 TCCATCCTCG ACACCATCTT CCACAAGGTG CTTTCTTCGG GCTGTGATTA TTCCGAACTC 540
 ACGTGGTACC TCACCTCCGT CTACCAGCAC AACCTCTTCT TCCTGCTGTC CCTGGGGATT 600

30 ATCCTGTTCT GCTACGTGGA GATCCTCAGG ACCCTGTTCC GCTCAGCTC CAAGCGGCGC 660
 CACCGCACGA AAAAGCTCAT CTTGCCATC GTGGTGGCCT ACTTCCTCAG CTGGGGTCCC 720
 TACAACTTCA CCCTGTTTCT GCAGACGCTG TTTCGGACCC AGATCATCCG GAGCTGCCAG 780

GCCAAACAGC AGCTAGAATA CGCCCTGCTC ATCTGCCGCA ACCTCGCCTT CTCCCACTGC 840
 TGCTTTAACC CGGTGCTCTA TGTCTTCGTG GGGGTCAAGT TCCGCACACA CCTGAAACAT 900
 GTTCTCCGGC AGTTCTGGTT CTGCCGGCTG CAGGCACCCA GCCCAGCCTC GATCCCCCAC 960
 TCCCCTGGTG CCTTCGCCTA TGAGGGCGCC TCCTTCTACT GA 1002

5 (169) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 333 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Met Glu Ser Ser Gly Asn Pro Glu Ser Thr Thr Phe Phe Tyr Tyr Asp
 1 5 10 15
 15 Leu Gln Ser Gln Pro Cys Glu Asn Gln Ala Trp Val Phe Ala Thr Leu
 20 25 30
 Ala Thr Thr Val Leu Tyr Cys Leu Val Phe Leu Leu Ser Leu Val Gly
 35 40 45
 20 Asn Ser Leu Val Leu Trp Val Leu Val Lys Tyr Glu Ser Leu Glu Ser
 50 55 60
 Leu Thr Asn Ile Phe Ile Leu Asn Leu Cys Leu Ser Asp Leu Val Phe
 65 70 75 80
 Ala Cys Leu Leu Pro Val Trp Ile Ser Pro Tyr His Trp Gly Trp Val
 85 90 95
 25 Leu Gly Asp Phe Leu Cys Lys Leu Leu Asn Met Ile Phe Ser Ile Ser
 100 105 110
 Leu Tyr Ser Ser Ile Phe Phe Leu Thr Ile Met Thr Ile His Arg Tyr
 115 120 125
 30 Leu Ser Val Val Ser Pro Leu Ser Thr Leu Arg Val Pro Thr Leu Arg
 130 135 140
 Cys Arg Val Leu Val Thr Met Ala Val Trp Val Ala Ser Ile Leu Ser
 145 150 155 160
 Ser Ile Leu Asp Thr Ile Phe His Lys Val Leu Ser Ser Gly Cys Asp
 165 170 175
 35 Tyr Ser Glu Leu Thr Trp Tyr Leu Thr Ser Val Tyr Gln His Asn Leu
 180 185 190

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Phe Phe Leu Leu Ser Leu Gly Ile Ile Leu Phe Cys Tyr Val Glu Ile
195 200 205

Leu Arg Thr Leu Phe Arg Ser Arg Ser Lys Arg Arg His Arg Thr Lys
210 215 220

5 Lys Leu Ile Phe Ala Ile Val Val Ala Tyr Phe Leu Ser Trp Gly Pro
225 230 235 240

Tyr Asn Phe Thr Leu Phe Leu Gln Thr Leu Phe Arg Thr Gln Ile Ile
245 250 255

10 Arg Ser Cys Glu Ala Lys Gln Gln Leu Glu Tyr Ala Leu Leu Ile Cys
260 265 270

Arg Asn Leu Ala Phe Ser His Cys Cys Phe Asn Pro Val Leu Tyr Val
275 280 285

Phe Val Gly Val Lys Phe Arg Thr His Leu Lys His Val Leu Arg Gln
290 295 300

15 Phe Trp Phe Cys Arg Leu Gln Ala Pro Ser Pro Ala Ser Ile Pro His
305 310 315 320

Ser Pro Gly Ala Phe Ala Tyr Glu Gly Ala Ser Phe Tyr
325 330

(170) INFORMATION FOR SEQ ID NO:169:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 987 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

ATGGACAACG CCTCGTTCTC GGAGCCCTGG CCCGCCAACG CATCGGGCCC GGACCCGGCG 60

CTGAGCTGCT CCAACGCGTC GACTCTGGCG CCGCTGCCGG CGCCGCTGGC GGTGGCTGTA 120

CCAGTTGTCT ACGCGGTGAT CTGCGCCGTG GGTCTGGCGG GCAACTCCGC CGTGCTGTAC 180

30 GTGTTGCTGC GGGCGCCCCG CATGAAGACC GTCACCAACC TGTTCATCCT CAACCTGGCC 240

ATCGCCGACG AGCTCTTCAC GCTGGTGCTG CCCATCAACA TCGCCGACTT CCTGCTGCGG 300

CAGTGGCCCT TCGGGGAGCT CATGTGCAAG CTCATCGTGG CTATCGACCA GTACAACACC 360

TTCTCCAGCC TCTACTTCCT CACCGTCATG AGCGCCGACC GCTACCTGGT GGTGTTGGCC 420

ACTGCGGAGT CGCGCCGGGT GGCCGGCCGC ACCTACAGCG CCGCGCGCGC GGTGAGCCTG 480

GCCGTGTGGG GGATCGTCAC ACTCGTCGTG CTGCCCTTCG CAGTCTTCGC CCGGCTAGAC 540
 GACGAGCAGG GCCGGCGCCA GTGCGTGCTA GTCTTTCCGC AGCCCGAGGC CTTCTGGTGG 600
 CGCGCGAGCC GCCTCTACAC GCTCGTGCTG GGCTTCGCCA TCCCCGTGTC CACCATCTGT 660
 GTCCTCTATA CCACCCTGCT GTGCCGGCTG CATGCCATGC GGCTGGACAG CCACGCCAAG 720
 5 GCCCTGGAGC GCGCCAAGAA GCGGGTGAAG TTCCTGGTGG TGGCAATCCT GGCGGTGTGC 780
 CTCCTCTGCT GGACGCCCTA CCACCTGAGC ACCGTGGTGG CGCTCACCAC CGACCTCCCG 840
 CAGACGCCGC TGTTCATCGC TATCTCTAC TTCATCACCA GCCTGACGTA CGCCAACAGC 900
 TGCCTCAACC CCTTCCTCTA CGCCTTCCTG GACGCCAGCT TCCGCAGGAA CCTCCGCCAG 960
 CTGATAACTT GCCGCGCGGC AGCCTGA 987

10 (171) INFORMATION FOR SEQ. ID NO:170:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 328 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 15 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Met Asp Asn Ala Ser Phe Ser Glu Pro Trp Pro Ala Asn Ala Ser Gly
 1 5 10 15
 20 Pro Asp Pro Ala Leu Ser Cys Ser Asn Ala Ser Thr Leu Ala Pro Leu
 20 25 30
 Pro Ala Pro Leu Ala Val Ala Val Pro Val Val Tyr Ala Val Ile Cys
 35 40 45
 25 Ala Val Gly Leu Ala Gly Asn Ser Ala Val Leu Tyr Val Leu Leu Arg
 50 55 60
 Ala Pro Arg Met Lys Thr Val Thr Asn Leu Phe Ile Leu Asn Leu Ala
 65 70 75 80
 Ile Ala Asp Glu Leu Phe Thr Leu Val Leu Pro Ile Asn Ile Ala Asp
 85 90 95
 30 Phe Leu Leu Arg Gln Trp Pro Phe Gly Glu Leu Met Cys Lys Leu Ile
 100 105 110
 Val Ala Ile Asp Gln Tyr Asn Thr Phe Ser Ser Leu Tyr Phe Leu Thr
 115 120 125
 Val Met Ser Ala Asp Arg Tyr Leu Val Val Leu Ala Thr Ala Glu Ser

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	130	135	140
	Arg Arg Val Ala Gly	Arg Thr Tyr Ser Ala Ala	Arg Ala Val Ser Leu
	145	150	155 160
5	Ala Val Trp Gly Ile Val Thr Leu Val Val Leu Pro Phe Ala Val Phe		
	165	170	175
	Ala Arg Leu Asp Asp Glu Gln Gly Arg Arg Gln Cys Val Leu Val Phe		
	180	185	190
	Pro Gln Pro Glu Ala Phe Trp Trp Arg Ala Ser Arg Leu Tyr Thr Leu		
	195	200	205
10	Val Leu Gly Phe Ala Ile Pro Val Ser Thr Ile Cys Val Leu Tyr Thr		
	210	215	220
	Thr Leu Leu Cys Arg Leu His Ala Met Arg Leu Asp Ser His Ala Lys		
	225	230	235 240
15	Ala Leu Glu Arg Ala Lys Lys Arg Val Lys Phe Leu Val Val Ala Ile		
	245	250	255
	Leu Ala Val Cys Leu Leu Cys Trp Thr Pro Tyr His Leu Ser Thr Val		
	260	265	270
	Val Ala Leu Thr Thr Asp Leu Pro Gln Thr Pro Leu Val Ile Ala Ile		
	275	280	285
20	Ser Tyr Phe Ile Thr Ser Leu Thr Tyr Ala Asn Ser Cys Leu Asn Pro		
	290	295	300
	Phe Leu Tyr Ala Phe Leu Asp Ala Ser Phe Arg Arg Asn Leu Arg Gln		
	305	310	315 320
25	Leu Ile Thr Cys Arg Ala Ala Ala		
	325		

(172) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1002 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

	ATGCAGGCCG CTGGGCACCC AGAGCCCCTT GACAGCAGGG GCTCCTTCTC CCTCCCCACG	60
35	ATGGGTGCCA ACGTCTCTCA GGACAATGGC ACTGGCCACA ATGCCACCTT CTCCGAGCCA	120
	CTGCCGTTCC TCTATGTGCT CCTGCCCGCC GTGTACTCCG GGATCTGTGC TGTGGGGCTG	180

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ACTGGCAACA CGGCCGTCAT CCTTGTAATC CTAAGGGCGC CCAAGATGAA GACGGTGACC 240
 AACGTGTTCA TCCTGAACCT GGCCGTCGCC GACGGGCTCT TCACGCTGGT ACTGCCTGTC 300
 AACATCGCGG AGCACCTGCT GCAGTACTGG CCCTTCGGGG AGCTGCTCTG CAAGCTGGTG 360
 CTGGCCGTCG ACCACTACAA CATCTTCTCC AGCATCTACT TCCTAGCCGT GATGAGCGTG 420
 5 GACCGATACC TGGTGGTGCT GGCCACCGTG AGGTCCCGCC ACATGCCCTG GCGCACCTAC 480
 CGGGGGGCGA AGGTCGCCAG CCTGTGTGTC TGGCTGGGCG TCACGGTCCT GGTCTGCCC 540
 TTCTTCTCTT TCGCTGGCGT CTACAGCAAC GAGCTGCAGG TCCAAGCTG TGGGCTGAGC 600
 TTCCCGTGGC CCGAGCAGGT CTGGTTCAAG GCCAGCCGTG TCTACACGTT GGTCTGGGC 660
 TTCGTGCTGC CCGTGTGCAC CATCTGTGTG CTCTACACAG ACCTCCTGCG CAGGCTGCGG 720
 10 GCCGTGCGGC TCCGCTCTGG AGCCAAGGT CTAGGCAAGG CCAGGCGGAA GGTGAAAGTC 780
 CTGGTCTCTG TCGTGCTGGC CGTGTGCCTC CTCTGTGGA CGCCCTTCCA CCTGGCCTCT 840
 GTCGTGGCCC TGACCACGGA CCTGCCCCAG ACCCACTGG TCATCAGTAT GTCCTACGTC 900
 ATCACCAGCC TCACGTACGC CAACTCGTGC CTGAACCCCT TCCTCTACGC CTTTCTAGAT 960
 GACAACTTCC GGAAGAACTT CCGCAGCATA TTGCGGTGCT GA 1002

15 (173) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

20

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Met Gln Ala Ala Gly His Pro Glu Pro Leu Asp Ser Arg Gly Ser Phe
 1 5 10 15
 25 Ser Leu Pro Thr Met Gly Ala Asn Val Ser Gln Asp Asn Gly Thr Gly
 20 25 30
 His Asn Ala Thr Phe Ser Glu Pro Leu Pro Phe Leu Tyr Val Leu Leu
 35 40 45
 30 Pro Ala Val Tyr Ser Gly Ile Cys Ala Val Gly Leu Thr Gly Asn Thr
 50 55 60
 Ala Val Ile Leu Val Ile Leu Arg Ala Pro Lys Met Lys Thr Val Thr
 65 70 75 80

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Asn Val Phe Ile Leu Asn Leu Ala Val Ala Asp Gly Leu Phe Thr Leu
 85 90 95
 Val Leu Pro Val Asn Ile Ala Glu His Leu Leu Gln Tyr Trp Pro Phe
 100 105 110
 5 Gly Glu Leu Leu Cys Lys Leu Val Leu Ala Val Asp His Tyr Asn Ile
 115 120 125
 Phe Ser Ser Ile Tyr Phe Leu Ala Val Met Ser Val Asp Arg Tyr Leu
 130 135 140
 10 Val Val Leu Ala Thr Val Arg Ser Arg His Met Pro Trp Arg Thr Tyr
 145 150 155 160
 Arg Gly Ala Lys Val Ala Ser Leu Cys Val Trp Leu Gly Val Thr Val
 165 170 175
 Leu Val Leu Pro Phe Phe Ser Phe Ala Gly Val Tyr Ser Asn Glu Leu
 180 185 190
 15 Gln Val Pro Ser Cys Gly Leu Ser Phe Pro Trp Pro Glu Gln Val Trp
 195 200 205
 Phe Lys Ala Ser Arg Val Tyr Thr Leu Val Leu Gly Phe Val Leu Pro
 210 215 220
 20 Val Cys Thr Ile Cys Val Leu Tyr Thr Asp Leu Leu Arg Arg Leu Arg
 225 230 235 240
 Ala Val Arg Leu Arg Ser Gly Ala Lys Ala Leu Gly Lys Ala Arg Arg
 245 250 255
 Lys Val Lys Val Leu Val Leu Val Val Leu Ala Val Cys Leu Leu Cys
 260 265 270
 25 Trp Thr Pro Phe His Leu Ala Ser Val Val Ala Leu Thr Thr Asp Leu
 275 280 285
 Pro Gln Thr Pro Leu Val Ile Ser Met Ser Tyr Val Ile Thr Ser Leu
 290 295 300
 30 Thr Tyr Ala Asn Ser Cys Leu Asn Pro Phe Leu Tyr Ala Phe Leu Asp
 305 310 315 320
 Asp Asn Phe Arg Lys Asn Phe Arg Ser Ile Leu Arg Cys
 325 330

(174) INFORMATION FOR SEQ ID NO:173:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1107 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

ATGGTCCTTG AGGTGAGTGA CCACCAAGTG CTAAATGACG CCGAGGTTGC CGCCCTCCTG 60
 GAGAACTTCA GCTCTTCCTA TGACTATGGA GAAAACGAGA GTGACTCGTG CTGTACCTCC 120
 5 CCGCCCTGCC CACAGGACTT CAGCCTGAAC TTCGACCGGG CCTTCCTGCC AGCCCTCTAC 180
 AGCCTCCTCT TTCTGCTGGG GCTGCTGGGC AACGGCGCGG TGGCAGCCGT GCTGCTGAGC 240
 CGGCGGACAG CCCTGAGCAG CACCGACACC TTCCTGCTCC ACCTAGCTGT AGCAGACACG 300
 CTGCTGGTGC TGACACTGCC GCTCTGGGCA GTGGACGCTG CCGTCCAGTG GGTCTTTGGC 360
 TCTGGCCTCT GCAAAGTGGC AGGTGCCCTC TTCAACATCA ACTTCTACGC AGGAGCCCTC 420
 10 CTGCTGGCCT GCATCAGCTT TGACCGCTAC CTGAACATAG TTCATGCCAC CCAGCTCTAC 480
 CGCCGGGGGC CCCC GGCCCG CGTGACCTC ACCTGCCTGG CTGTCTGGGG GCTCTGCCTG 540
 CTTTTCGCCC TCCCAGACTT CATCTTCCTG TCGGCCCACC ACGACGAGCG CCTCAACGCC 600
 ACCCACTGCC AATACAACTT CCCACAGGTG GGCCGCACGG CTCTGCGGGT GCTGCAGCTG 660
 GTGGCTGGCT TTCTGCTGCC CTTGCTGGTC ATGGCCTACT GCTATGCCCA CATCCTGGCC 720
 15 GTGCTGCTGG TTTCCAGGGG CCAGCGGCGC CTGCGGGCCA AGCGGCTGGT GGTGGTGGTC 780
 GTGGTGGCCT TTGCCCTCTG CTGGACCCCC TATCACCTGG TGGTGTGGT GGACATCCTC 840
 ATGGACCTGG GCGCTTTGGC CCGCAACTGT GGCCGAGAAA GCAGGGTAGA CGTGGCCAAG 900
 TCGGTCACCT CAGGCCTGGG CTACATGCAC TGCTGCCTCA ACCCGCTGCT CTATGCCTTT 960
 GTAGGGGTCA AGTTCCGGGA GCGGATGTGG ATGCTGCTCT TGCGCCTGGG CTGCCCCAAC 1020
 20 CAGAGAGGGC TCCAGAGGCA GCCATCGTCT TCCCGCCGGG ATTCATCCTG GTCTGAGACC 1080
 TCAGAGGCCT CCTACTCGGG CTTGTGA 1107

(175) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

124

	Met	Val	Leu	Glu	Val	Ser	Asp	His	Gln	Val	Leu	Asn	Asp	Ala	Glu	Val	
	1				5					10					15		
	Ala	Ala	Leu	Leu	Glu	Asn	Phe	Ser	Ser	Ser	Tyr	Asp	Tyr	Gly	Glu	Asn	
			20						25					30			
5	Glu	Ser	Asp	Ser	Cys	Cys	Thr	Ser	Pro	Pro	Cys	Pro	Gln	Asp	Phe	Ser	
			35					40					45				
	Leu	Asn	Phe	Asp	Arg	Ala	Phe	Leu	Pro	Ala	Leu	Tyr	Ser	Leu	Leu	Phe	
		50					55					60					
10	Leu	Leu	Gly	Leu	Leu	Gly	Asn	Gly	Ala	Val	Ala	Ala	Val	Leu	Leu	Ser	
	65				70						75					80	
	Arg	Arg	Thr	Ala	Leu	Ser	Ser	Thr	Asp	Thr	Phe	Leu	Leu	His	Leu	Ala	
					85					90					95		
	Val	Ala	Asp	Thr	Leu	Leu	Val	Leu	Thr	Leu	Pro	Leu	Trp	Ala	Val	Asp	
				100					105					110			
15	Ala	Ala	Val	Gln	Trp	Val	Phe	Gly	Ser	Gly	Leu	Cys	Lys	Val	Ala	Gly	
			115					120					125				
	Ala	Leu	Phe	Asn	Ile	Asn	Phe	Tyr	Ala	Gly	Ala	Leu	Leu	Leu	Ala	Cys	
		130					135					140					
20	Ile	Ser	Phe	Asp	Arg	Tyr	Leu	Asn	Ile	Val	His	Ala	Thr	Gln	Leu	Tyr	
	145					150					155					160	
	Arg	Arg	Gly	Pro	Pro	Ala	Arg	Val	Thr	Leu	Thr	Cys	Leu	Ala	Val	Trp	
					165					170					175		
	Gly	Leu	Cys	Leu	Leu	Phe	Ala	Leu	Pro	Asp	Phe	Ile	Phe	Leu	Ser	Ala	
			180						185					190			
25	His	His	Asp	Glu	Arg	Leu	Asn	Ala	Thr	His	Cys	Gln	Tyr	Asn	Phe	Pro	
			195					200					205				
	Gln	Val	Gly	Arg	Thr	Ala	Leu	Arg	Val	Leu	Gln	Leu	Val	Ala	Gly	Phe	
		210					215					220					
30	Leu	Leu	Pro	Leu	Leu	Val	Met	Ala	Tyr	Cys	Tyr	Ala	His	Ile	Leu	Ala	
	225					230					235					240	
	Val	Leu	Leu	Val	Ser	Arg	Gly	Gln	Arg	Arg	Leu	Arg	Ala	Lys	Arg	Leu	
				245						250					255		
	Val	Val	Val	Val	Val	Val	Ala	Phe	Ala	Leu	Cys	Trp	Thr	Pro	Tyr	His	
				260				265						270			
35	Leu	Val	Val	Leu	Val	Asp	Ile	Leu	Met	Asp	Leu	Gly	Ala	Leu	Ala	Arg	
			275					280					285				
	Asn	Cys	Gly	Arg	Glu	Ser	Arg	Val	Asp	Val	Ala	Lys	Ser	Val	Thr	Ser	

125

290 295 300

Gly Leu Gly Tyr Met His Cys Cys Leu Asn Pro Leu Leu Tyr Ala Phe
305 310 315 320

Val Gly Val Lys Phe Arg Glu Arg Met Trp Met Leu Leu Leu Arg Leu
325 330 335

Gly Cys Pro Asn Gln Arg Gly Leu Gln Arg Gln Pro Ser Ser Ser Arg
340 345 350

Arg Asp Ser Ser Trp Ser Glu Thr Ser Glu Ala Ser Tyr Ser Gly Leu
355 360 365

10 (176) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1074 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

ATGGCTGATG ACTATGGCTC TGAATCCACA TCTTCCATGG AAGACTACGT TAACTTCAAC 60

TTCCTGACT TCTACTGTGA GAAAAACAAT GTCAGGCAGT TTGCGAGCCA TTCCTCCCA 120

20 CCCTTGACT GGCTCGTGT CATCGTGGGT GCCTTGGGCA ACAGTCTTGT TATCCTTGTC 180

TACTGGTACT GCACAAGAGT GAAGACCATG ACCGACATGT TCCTTTTGAA TTTGGCAATT 240

GCTGACCTCC TCTTTCTTGT CACTCTTCCC TTCTGGGCCA TTGCTGCTGC TGACCAGTGG 300

AAGTTCCAGA CCTTCATGTG CAAGGTGGTC AACAGCATGT ACAAGATGAA CTCTACAGC 360

TGTGTGTTGC TGATCATGTG CATCAGCGTG GACAGGTACA TTGCCATTGC CCAGGCCATG 420

25 AGAGCACATA CTTGGAGGGA GAAAAGGCTT TTGTACAGCA AAATGGTTTG CTTTACCATC 480

TGGGTATTGG CAGCTGCTCT CTGCATCCCA GAAATCTTAT ACAGCCAAAT CAAGGAGGAA 540

TCCGGCATTG CTATCTGCAC CATGGTTTAC CCTAGCGATG AGAGCACCAA ACTGAAGTCA 600

GCTGTCTTGA CCCTGAAGGT CATCTGGGG TTCTTCCTTC CCTTCGTGGT CATGGCTTGC 660

TGCTATACCA TCATCATTCA CACCCTGATA CAAGCCAAGA AGTCTTCCAA GCACAAAGCC 720

30 AAGAAAGTGA CCATCACTGT CCTGACCGTC TTTGTCTTGT CTCAGTTTCC CTACAAGTGC 780

ATTTTGTGG TGCAGACCAT TGACGCCTAT GCCATGTTCA TCTCCAAGT TGCCGTTTCC 840

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ACCAACATTG ACATCTGCTT CCAGGTCACC CAGACCATCG CCTTCTTCCA CAGTTGCCTG 900
 AACCCCTGTTT TCTATGTTTT TGTGGGTGAG AGATTCCGCC GGGATCTCGT GAAAACCCCTG 960
 AAGAACTTGG GTTGATCAG CCAGGCCAG TGGGTTTCAT TTACAAGGAG AGAGGGAAGC 1020
 TTGAAGCTGT CGTCTATGTT GCTGGAGACA ACCTCAGGAG CACTCTCCCT CTGA 1074

5 (177) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

10

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Met Ala Asp Asp Tyr Gly Ser Glu Ser Thr Ser Ser Met Glu Asp Tyr
 1 5 10 15
 Val Asn Phe Asn Phe Thr Asp Phe Tyr Cys Glu Lys Asn Asn Val Arg
 20 25 30
 Gln Phe Ala Ser His Phe Leu Pro Pro Leu Tyr Trp Leu Val Phe Ile
 35 40 45
 Val Gly Ala Leu Gly Asn Ser Leu Val Ile Leu Val Tyr Trp Tyr Cys
 50 55 60
 Thr Arg Val Lys Thr Met Thr Asp Met Phe Leu Leu Asn Leu Ala Ile
 65 70 75 80
 Ala Asp Leu Leu Phe Leu Val Thr Leu Pro Phe Trp Ala Ile Ala Ala
 85 90 95
 Ala Asp Gln Trp Lys Phe Gln Thr Phe Met Cys Lys Val Val Asn Ser
 100 105 110
 Met Tyr Lys Met Asn Phe Tyr Ser Cys Val Leu Leu Ile Met Cys Ile
 115 120 125
 Ser Val Asp Arg Tyr Ile Ala Ile Ala Gln Ala Met Arg Ala His Thr
 130 135 140
 Trp Arg Glu Lys Arg Leu Leu Tyr Ser Lys Met Val Cys Phe Thr Ile
 145 150 155 160
 Trp Val Leu Ala Ala Ala Leu Cys Ile Pro Glu Ile Leu Tyr Ser Gln
 165 170 175
 Ile Lys Glu Glu Ser Gly Ile Ala Ile Cys Thr Met Val Tyr Pro Ser
 180 185 190

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Asp Glu Ser Thr Lys Leu Lys Ser Ala Val Leu Thr Leu Lys Val Ile
 195 200 205
 Leu Gly Phe Phe Leu Pro Phe Val Val Met Ala Cys Cys Tyr Thr Ile
 210 215 220
 5 Ile Ile His Thr Leu Ile Gln Ala Lys Lys Ser Ser Lys His Lys Ala
 225 230 235 240
 Lys Lys Val Thr Ile Thr Val Leu Thr Val Phe Val Leu Ser Gln Phe
 245 250 255
 10 Pro Tyr Asn Cys Ile Leu Leu Val Gln Thr Ile Asp Ala Tyr Ala Met
 260 265 270
 Phe Ile Ser Asn Cys Ala Val Ser Thr Asn Ile Asp Ile Cys Phe Gln
 275 280 285
 Val Thr Gln Thr Ile Ala Phe Phe His Ser Cys Leu Asn Pro Val Leu
 290 295 300
 15 Tyr Val Phe Val Gly Glu Arg Phe Arg Arg Asp Leu Val Lys Thr Leu
 305 310 315 320
 Lys Asn Leu Gly Cys Ile Ser Gln Ala Gln Trp Val Ser Phe Thr Arg
 325 330 335
 20 Arg Glu Gly Ser Leu Lys Leu Ser Ser Met Leu Leu Glu Thr Thr Ser
 340 345 350
 Gly Ala Leu Ser Leu
 355

(178) INFORMATION FOR SEQ ID NO:177:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1110 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

ATGGCCTCAT CGACCACTCG GGGCCCCAGG GTTCTGACT TATTTCTGG GCTGCCGCCG 60
 GCGGTCACAA CTCCGCGCAA CCAGAGCGCA GAGGCCTCGG CGGGCAACGG GTCGGTGGCT 120
 GGCGCGGACG CTCCAGCCGT CACGCCCTTC CAGAGCCTGC AGCTGGTGCA TCAGCTGAAG 180
 GGGCTGATCG TGCTGCTCTA CAGCGTCGTG GTGGTCGTGG GGCTGGTGGG CAACTGCCTG 240
 35 CTGGTGCTGG TGATCGCGCG GGTGCCGCGG CTGCACAACG TGACGAACTT CCTCATCGGC 300

AACCTGGCCT TGTCCGACGT GTCATGTGC ACCGCCTGCG TGCCGCTCAC GCTGGCCTAT 360
 GCCTTCGAGC CACGCGGCTG GGTGTTTCGGC GGC GGCCCTGT GCCACCTGGT CTTCTTCCTG 420
 CAGCCGGTCA CCGTCTATGT GTCGGTGTTC ACGCTCACCA CCATCGCAGT GGACCGCTAC 480
 GTCGTGCTGG TGCACCCGCT GAGGCGCGCA TCTCGCTGCG CCTCAGCCTA CGCTGTGCTG 540
 5 GCCATCTGGG CGCTGTCCGC GGTGCTGGCG CTGCCGCCCG CCGTGCACAC CTATCACGTG 600
 GAGCTCAAGC CGCACGACGT GCGCCTCTGC GAGGAGTTCT GGGGCTCCCA GGAGCGCCAG 660
 CGCCAGCTCT ACGCCTGGGG GCTGCTGCTG GTCACCTACC TGCTCCCTCT GCTGGTCATC 720
 CTCCTGTCTT ACGTCCGGGT GTCAGTGAAG CTCCGCAACC GCGTGGTGCC GGGCTGCGTG 780
 ACCCAGAGCC AGGCCGACTG GGACCGCGCT CGGCGCCGGC GCACCAAATG CTTGCTGGTG 840
 10 GTGGTCGTGG TGGTGTTCGC CGTCTGCTGG CTGCCGCTGC ACGTCTTCAA CCTGCTGCGG 900
 GACCTCGACC CCCACGCCAT CGACCCTTAC GCCTTTGGGC TGGTGCAGCT GCTCTGCCAC 960
 TGGCTCGCCA TGAGTTCGGC CTGCTACAAC CCCTTCATCT ACGCCTGGCT GCACGACAGC 1020
 TTCCGCGAGG AGCTGCGCAA ACTGTTGGTC GCTTGGCCCC GCAAGATAGC CCCCCATGGC 1080
 CAGAATATGA CCGTCAGCGT GGTCACTCTGA 1110

15 (179) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 369 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

20 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

Met Ala Ser Ser Thr Thr Arg Gly Pro Arg Val Ser Asp Leu Phe Ser
 1 5 10 15
 25 Gly Leu Pro Pro Ala Val Thr Thr Pro Ala Asn Gln Ser Ala Glu Ala
 20 25 30
 Ser Ala Gly Asn Gly Ser Val Ala Gly Ala Asp Ala Pro Ala Val Thr
 35 40 45
 30 Pro Phe Gln Ser Leu Gln Leu Val His Gln Leu Lys Gly Leu Ile Val
 50 55 60
 Leu Leu Tyr Ser Val Val Val Val Val Gly Leu Val Gly Asn Cys Leu
 65 70 75 80

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Leu Val Leu Val Ile Ala Arg Val Pro Arg Leu His Asn Val Thr Asn
 85 90 95
 Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu Met Cys Thr Ala
 100 105 110
 5 Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly Trp Val
 115 120 125
 Phe Gly Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Pro Val Thr
 130 135 140
 10 Val Tyr Val Ser Val Phe Thr Leu Thr Thr Ile Ala Val Asp Arg Tyr
 145 150 155 160
 Val Val Leu Val His Pro Leu Arg Arg Ala Ser Arg Cys Ala Ser Ala
 165 170 175
 Tyr Ala Val Leu Ala Ile Trp Ala Leu Ser Ala Val Leu Ala Leu Pro
 180 185 190
 15 Pro Ala Val His Thr Tyr His Val Glu Leu Lys Pro His Asp Val Arg
 195 200 205
 Leu Cys Glu Glu Phe Trp Gly Ser Gln Glu Arg Gln Arg Gln Leu Tyr
 210 215 220
 20 Ala Trp Gly Leu Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val Ile
 225 230 235 240
 Leu Leu Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg Val Val
 245 250 255
 Pro Gly Cys Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg Arg
 260 265 270
 25 Arg Arg Thr Lys Cys Leu Leu Val Val Val Val Val Val Phe Ala Val
 275 280 285
 Cys Trp Leu Pro Leu His Val Phe Asn Leu Leu Arg Asp Leu Asp Pro
 290 295 300
 30 His Ala Ile Asp Pro Tyr Ala Phe Gly Leu Val Gln Leu Leu Cys His
 305 310 315 320
 Trp Leu Ala Met Ser Ser Ala Cys Tyr Asn Pro Phe Ile Tyr Ala Trp
 325 330 335
 Leu His Asp Ser Phe Arg Glu Glu Leu Arg Lys Leu Leu Val Ala Trp
 340 345 350
 35 Pro Arg Lys Ile Ala Pro His Gly Gln Asn Met Thr Val Ser Val Val
 355 360 365
 Ile

(180) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1083 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

10 ATGGACCCAG AAGAACTTC AGTTATTG GATTATTACT ATGCTACGAG CCCAACTCT 60
GACATCAGGG AGACCCACTC CCATGTTCTT TACACCTCTG TCTTCCTTCC AGTCTTTTAC 120
ACAGCTGTGT TCCTGACTGG AGTGCTGGGG AACCTTGTTT TCATGGGAGC GTTGCAATTC 180
AAACCCGGCA GCCGAAGACT GATCGACATC TTTATCATCA ATCTGGCTGC CTCTGACTTC 240
ATTTTTCTTG TCACATTGCC TCTCTGGGTG GATAAAGAAG CATCTCTAGG ACTGTGGAGG 300
15 ACGGGCTCCT TCCTGTGCAA AGGGAGCTCC TACATGATCT CCGTCAATAT GCACTGCAGT 360
GTCCTCCTGC TCACTTGCAAT GAGTGTTGAC CGCTACCTGG CCATTGTGTG GCCAGTCGTA 420
TCCAGGAAAT TCAGAAGGAC AGACTGTGCA TATGTAGTCT GTGCCAGCAT CTGGTTTATC 480
TCCTGCCTGC TGGGGTTGCC TACTCTTCTG TCCAGGGAGC TCACGCTGAT TGATGATAAG 540
CCATACTGTG CAGAGAAAAA GGCAACTCCA ATTAACTCA TATGGTCCCT GGTGGCCTTA 600
20 ATTTTCACCT TTTTGTCCC TTTGTTGAGC ATTGTGACCT GCTACTGTTG CATTGCAAGG 660
AAGCTGTGTG CCCATTACCA GCAATCAGGA AAGCACAACA AAAAGCTGAA GAAATCTAAG 720
AAGATCATCT TTATTGTCGT GGCAGCCTTT CTTGTCTCCT GGCTGCCCTT CAATACTTTC 780
AAGTTCCTGG CCATTGTCTC TGGGTTGCGG CAAGAACACT ATTTACCCCTC AGCTATTCTT 840
CAGCTTGGTA TGGAGGTGAG TGGACCCTTG GCATTTGCCA ACAGCTGTGT CAACCCCTTC 900
25 ATTTACTATA TCTTCGACAG CTACATCCGC CGGGCCATTG TCCACTGCTT GTGCCCTTGC 960
CTGAAAAACT ATGACTTTGG GAGTAGCACT GAGACATCAG ATAGTCACCT CACTAAGGCT 1020
CTCTCCACCT TCATTCATGC AGAAGATTTT GCCAGGAGGA GGAAGAGGTC TGTGTCACTC 1080
TAA 1083

(181) INFORMATION FOR SEQ ID NO:180:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 amino acids

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(B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii). MOLECULE TYPE: protein

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

```

Met Asp Pro Glu Glu Thr Ser Val Tyr Leu Asp Tyr Tyr Tyr Ala Thr
1           5           10           15

Ser Pro Asn Ser Asp Ile Arg Glu Thr His Ser His Val Pro Tyr Thr
          20           25           30

10 Ser Val Phe Leu Pro Val Phe Tyr Thr Ala Val Phe Leu Thr Gly Val
    35           40           45

Leu Gly Asn Leu Val Leu Met Gly Ala Leu His Phe Lys Pro Gly Ser
    50           55           60

15 Arg Arg Leu Ile Asp Ile Phe Ile Ile Asn Leu Ala Ala Ser Asp Phe
    65           70           75           80

Ile Phe Leu Val Thr Leu Pro Leu Trp Val Asp Lys Glu Ala Ser Leu
          85           90           95

Gly Leu Trp Arg Thr Gly Ser Phe Leu Cys Lys Gly Ser Ser Tyr Met
          100          105          110

20 Ile Ser Val Asn Met His Cys Ser Val Leu Leu Leu Thr Cys Met Ser
    115          120          125

Val Asp Arg Tyr Leu Ala Ile Val Trp Pro Val Val Ser Arg Lys Phe
    130          135          140

25 Arg Arg Thr Asp Cys Ala Tyr Val Val Cys Ala Ser Ile Trp Phe Ile
    145          150          155          160

Ser Cys Leu Leu Gly Leu Pro Thr Leu Leu Ser Arg Glu Leu Thr Leu
          165          170          175

Ile Asp Asp Lys Pro Tyr Cys Ala Glu Lys Lys Ala Thr Pro Ile Lys
          180          185          190

30 Leu Ile Trp Ser Leu Val Ala Leu Ile Phe Thr Phe Phe Val Pro Leu
    195          200          205

Leu Ser Ile Val Thr Cys Tyr Cys Cys Ile Ala Arg Lys Leu Cys Ala
    210          215          220

35 His Tyr Gln Gln Ser Gly Lys His Asn Lys Lys Leu Lys Lys Ser Lys
    225          230          235          240

Lys Ile Ile Phe Ile Val Val Ala Ala Phe Leu Val Ser Trp Leu Pro
          245          250          255

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Phe Asn Thr Phe Lys Phe Leu Ala Ile Val Ser Gly Leu Arg Gln Glu
 260 265 270
 His Tyr Leu Pro Ser Ala Ile Leu Gln Leu Gly Met Glu Val Ser Gly
 275 280 285
 5 Pro Leu Ala Phe Ala Asn Ser Cys Val Asn Pro Phe Ile Tyr Tyr Ile
 290 295 300
 Phe Asp Ser Tyr Ile Arg Arg Ala Ile Val His Cys Leu Cys Pro Cys
 305 310 315 320
 10 Leu Lys Asn Tyr Asp Phe Gly Ser Ser Thr Glu Thr Ser Asp Ser His
 325 330 335
 Leu Thr Lys Ala Leu Ser Thr Phe Ile His Ala Glu Asp Phe Ala Arg
 340 345 350
 Arg Arg Lys Arg Ser Val Ser Leu
 355 360
 15 (182) INFORMATION FOR SEQ ID NO:181:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1020 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 20 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:
 ATGAATGGCC TTGAAGTGGC TCCCCAGGT CTGATCACCA ACTTCTCCCT GGCCACGGCA 60
 GAGCAATGTG GCCAGGAGAC GCCACTGGAG AACATGCTGT TCGCCTCCTT CTACCTTCTG 120
 25 GATTTTATCC TGGCTTTAGT TGGCAATACC CTGGCTCTGT GGCTTTTCAT CCGAGACCAC 180
 AAGTCCGGGA CCCC GGCCAA CGTGTTCTCTG ATGCATCTGG CCGTGGCCGA CTTGTCGTGC 240
 GTGCTGGTCC TGCCACCCG CCTGGTCTAC CACTTCTCTG GGAACCACTG GCCATTTGGG 300
 GAAATCGCAT GCCGTCTCAC CGGCTTCCTC TTCTACCTCA ACATGTACGC CAGCATCTAC 360
 TTCCTCACCT GCATCAGCGC CGACCGTTTC CTGGCCATTG TGCACCCGGT CAAGTCCCTC 420
 30 AAGCTCCGCA GGCCCTCTA CGCACACCTG GCCTGTGCCT TCCTGTGGGT GGTGGTGGCT 480
 GTGGCCATGG CCCC GCTGCT GGTGAGCCCA CAGACCGTGC AGACCAACCA CACGGTGGTC 540
 TGCCTGCAGC TGTACCGGGA GAAGGCCTCC CACCATGCCC TGGTGTCCCT GGCACTGGCC 600
 TTCACCTTCC CGTTCATCAC CACGGTCACC TGCTACCTGC TGATCATCCG CAGCCTGCGG 660

133

CAGGGCCTGC GTGTGGAGAA GCGCCTCAAG ACCAAGGCAA AACGCATGAT CGCCATAGTG 720
 CTGGCCATCT TCCTGGTCTG CTTCTGTCCC TACCACGTCA ACCGCTCCGT CTACGTGCTG 780
 CACTACCGCA GCCATGGGGC CTCCTGCGCC ACCCAGCGCA TCCTGGCCCT GGCAAACCGC 840
 ATCACCTCCT GCCTCACCAG CCTCAACGGG GCACTCGACC CCATCATGTA TTTCTTCGTG 900
 5 GCTGAGAAGT TCCGCCACGC CCTGTGCAAC TTGCTCTGTG GCAAAGGCT CAAGGGCCCG 960
 CCCCCAGCT TCGAAGGGAA AACCAACGAG AGCTCGCTGA GTGCAAGTC AGAGCTGTGA 1020

(183) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 339 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

15

Met Asn Gly Leu Glu Val Ala Pro Pro Gly Leu Ile Thr Asn Phe Ser
 1 5 10 15

Leu Ala Thr Ala Glu Gln Cys Gly Gln Glu Thr Pro Leu Glu Asn Met
 20 25 30

20

Leu Phe Ala Ser Phe Tyr Leu Leu Asp Phe Ile Leu Ala Leu Val Gly
 35 40 45

Asn Thr Leu Ala Leu Trp Leu Phe Ile Arg Asp His Lys Ser Gly Thr
 50 55 60

Pro Ala Asn Val Phe Leu Met His Leu Ala Val Ala Asp Leu Ser Cys
 65 70 75 80

25

Val Leu Val Leu Pro Thr Arg Leu Val Tyr His Phe Ser Gly Asn His
 85 90 95

Trp Pro Phe Gly Glu Ile Ala Cys Arg Leu Thr Gly Phe Leu Phe Tyr
 100 105 110

30

Leu Asn Met Tyr Ala Ser Ile Tyr Phe Leu Thr Cys Ile Ser Ala Asp
 115 120 125

Arg Phe Leu Ala Ile Val His Pro Val Lys Ser Leu Lys Leu Arg Arg
 130 135 140

Pro Leu Tyr Ala His Leu Ala Cys Ala Phe Leu Trp Val Val Val Ala
 145 150 155 160

35

Val Ala Met Ala Pro Leu Leu Val Ser Pro Gln Thr Val Gln Thr Asn

134

		165		170		175
	His Thr Val	Val Cys Leu Gln Leu Tyr Arg Glu Lys Ala Ser His His				
		180		185		190
5	Ala Leu Val	Ser Leu Ala Val Ala Phe Thr Phe Pro Phe Ile Thr Thr				
		195		200		205
	Val Thr Cys Tyr	Leu Leu Ile Ile Arg Ser Leu Arg Gln Gly Leu Arg				
		210		215		220
	Val Glu Lys Arg	Leu Lys Thr Lys Ala Lys Arg Met Ile Ala Ile Val				
		225		230		235
10	Leu Ala Ile Phe	Leu Val Cys Phe Val Pro Tyr His Val Asn Arg Ser				
		245		250		255
	Val Tyr Val Leu	His Tyr Arg Ser His Gly Ala Ser Cys Ala Thr Gln				
		260		265		270
15	Arg Ile Leu Ala	Leu Ala Asn Arg Ile Thr Ser Cys Leu Thr Ser Leu				
		275		280		285
	Asn Gly Ala Leu	Asp Pro Ile Met Tyr Phe Phe Val Ala Glu Lys Phe				
		290		295		300
	Arg His Ala Leu	Cys Asn Leu Leu Cys Gly Lys Arg Leu Lys Gly Pro				
		305		310		315
20	Pro Pro Ser Phe	Glu Gly Lys Thr Asn Glu Ser Ser Leu Ser Ala Lys				
		325		330		335
	Ser Glu Leu					

(183) INFORMATION FOR SEQ ID NO:183:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 996 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 30 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

ATGATCACCC	TGAACAATCA	AGATCAACCT	GTCCCTTTTA	ACAGCTCACA	TCCAGATGAA	60
TACAAAATTG	CAGCCCTTGT	CTTCTATAGC	TGTATCTTCA	TAATTGGATT	ATTTGTTAAC	120
ATCACTGCAT	TATGGGTTTT	CAGTTGTACC	ACCAAGAAGA	GAACCACGGT	AACCATCTAT	180
35 ATGATGAATG	TGGCATTAGT	GGACTTGATA	TTTATAATGA	CTTTACCCTT	TCGAATGTTT	240

135

TATTATGCAA AAGATGAATG GCCATTTGGA GAGTACTTCT GCCAGATTCT TGGAGCTCTC 300
 ACAGTGTTTT ACCCAAGCAT TGCTTTATGG CTTCTTGCCT TTATTAGTGC TGACAGATAC 360
 ATGGCCATTG TACAGCCGAA GTACGCCAAA GAACTTAAAA ACACGTGCAA AGCCGTGCTG 420
 GCGTGTGTGG GAGTCTGGAT AATGACCCTG ACCACGACCA CCCCTCTGCT ACTGCTCTAT 480
 5 AAAGACCCAG ATAAAGACTC CACTCCCGCC ACCTGCCTCA AGATTTCTGA CATCATCTAT 540
 CTAAAAGCTG TGAACGTGCT GAACCTCACT CGACTGACAT TTTTTTCTT GATTCTTTG 600
 TTCATCATGA TTGGGTGCTA CTTGGTCATT ATTCATAATC TCCTTCACGG CAGGACGTCT 660
 AAGCTGAAAC CCAAAGTCAA GGAGAAGTCC AAAAGGATCA TCATCACGCT GCTGGTGCAG 720
 GTGCTCGTCT GCTTTATGCC CTTCCACATC TGTTTCGCTT TCCTGATGCT GGGAACGGGG 780
 10 GAGAATAGTT ACAATCCCTG GGGAGCCTTT ACCACCTTCC TCATGAACCT CAGCACGTGT 840
 CTGGATGTGA TTCTCTACTA CATCGTTTCA AAACAATTTT AGGCTCGAGT CATTAGTGTC 900
 ATGCTATACC GTAATTACCT TCGAAGCATG CGCAGAAAAA GTTTCCGATC TGGTAGTCTA 960
 AGGTCATAA GCAATATAAA CAGTGAAATG TTATGA 996

(185) INFORMATION FOR SEQ ID NO:184:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 331 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

20 (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Met	Ile	Thr	Leu	Asn	Asn	Gln	Asp	Gln	Pro	Val	Pro	Phe	Asn	Ser	Ser	1	5	10	15
His	Pro	Asp	Glu	Tyr	Lys	Ile	Ala	Ala	Leu	Val	Phe	Tyr	Ser	Cys	Ile	20	25	30	
Phe	Ile	Ile	Gly	Leu	Phe	Val	Asn	Ile	Thr	Ala	Leu	Trp	Val	Phe	Ser	35	40	45	
Cys	Thr	Thr	Lys	Lys	Arg	Thr	Thr	Val	Thr	Ile	Tyr	Met	Met	Asn	Val	50	55	60	
Ala	Leu	Val	Asp	Leu	Ile	Phe	Ile	Met	Thr	Leu	Pro	Phe	Arg	Met	Phe	65	70	75	80
Tyr	Tyr	Ala	Lys	Asp	Glu	Trp	Pro	Phe	Gly	Glu	Tyr	Phe	Cys	Gln	Ile	85	90	95	

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Leu Gly Ala Leu Thr Val Phe Tyr Pro Ser Ile Ala Leu Trp Leu Leu
 100 105 110
 Ala Phe Ile Ser Ala Asp Arg Tyr Met Ala Ile Val Gln Pro Lys Tyr
 115 120 125
 5 Ala Lys Glu Leu Lys Asn Thr Cys Lys Ala Val Leu Ala Cys Val Gly
 130 135 140
 Val Trp Ile Met Thr Leu Thr Thr Thr Thr Pro Leu Leu Leu Tyr
 145 150 155 160
 10 Lys Asp Pro Asp Lys Asp Ser Thr Pro Ala Thr Cys Leu Lys Ile Ser
 165 170 175
 Asp Ile Ile Tyr Leu Lys Ala Val Asn Val Leu Asn Leu Thr Arg Leu
 180 185 190
 Thr Phe Phe Phe Leu Ile Pro Leu Phe Ile Met Ile Gly Cys Tyr Leu
 195 200 205
 15 Val Ile Ile His Asn Leu Leu His Gly Arg Thr Ser Lys Leu Lys Pro
 210 215 220
 Lys Val Lys Glu Lys Ser Lys Arg Ile Ile Ile Thr Leu Leu Val Gln
 225 230 235 240
 20 Val Leu Val Cys Phe Met Pro Phe His Ile Cys Phe Ala Phe Leu Met
 245 250 255
 Leu Gly Thr Gly Glu Asn Ser Tyr Asn Pro Trp Gly Ala Phe Thr Thr
 260 265 270
 Phe Leu Met Asn Leu Ser Thr Cys Leu Asp Val Ile Leu Tyr Tyr Ile
 275 280 285
 25 Val Ser Lys Gln Phe Gln Ala Arg Val Ile Ser Val Met Leu Tyr Arg
 290 295 300
 Asn Tyr Leu Arg Ser Met Arg Arg Lys Ser Phe Arg Ser Gly Ser Leu
 305 310 315 320
 30 Arg Ser Leu Ser Asn Ile Asn Ser Glu Met Leu
 325 330

(186) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1077 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

ATGCCCTCTG TGTCTCCAGC GGGGCCCTCG GCCGGGGCAG TCCCAATGC CACCGCAGTG 60
 ACAACAGTGC GGACCAATGC CAGCGGGCTG GAGGTGCCCC GTTCCACCT GTTTGCCCCG 120
 CTGGACGAGG AGCTGCATGG CACCTTCCCA GGCCTGTGCG TGGCGCTGAT GGCGGTGCAC 180
 5 GGAGCCATCT TCCTGGCAGG GCTGGTGCTC AACGGGCTGG CGCTGTACGT CTTCTGCTGC 240
 CGCACC CGG CCAAGACACC CTCAGTCATC TACACCATCA ACCTGGTGGT GACCGATCTA 300
 CTGGTAGGGC TGTCCCTGCC CACGCGCTTC GCTGTGTACT ACGGCGCCAG GGGCTGCCTG 360
 CGCTGTGCCT TCCCGCACGT CCTCGGTTAC TTCCTCAACA TGCCTGCTC CATCCTCTTC 420
 CTCACCTGCA TCTGCGTGGA CCGCTACCTG GCCATCGTGC GGCCCGAAGG CTCCCGCCGC 480
 10 TGCCGCCAGC CTGCCTGTGC CAGGGCCGTG TCGCCTTCG TGTGGCTGGC CGCCGGTGCC 540
 GTCACCCTGT CGGTGTGTTG CGTGACAGGC AGCCGGCCCT GTCGCCGTGT CTTTGCGCTG 600
 ACTGTCCTGG AGTTCCTGCT GCCCTGCTG GTCATCAGCG TGTTTACCG CCGCATCATG 660
 TGTGCACTGT CGCGGCCGG TCTGCTCCAC CAGGGTCGCC AGCGCCGCGT GCGGGCCAAG 720
 CAGCTCCTGC TCACGGTGCT CATCATCTTT CTCGTCTGCT TCACGCCCTT CCACGCCCGC 780
 15 CAAGTGGCCG TGGCGCTGTG GCGGACATG CCACACCACA CGAGCCTCGT GGTCTACCAC 840
 GTGGCCGTGA CCCTCAGCAG CCTCAACAGC TGCATGGACC CCATCGTCTA CTGCTTCGTC 900
 ACCAGTGGCT TCCAGGCCAC CGTCCGAGGC CTCTTCGGCC AGCACGGAGA GCGTGAGCCC 960
 AGCAGCGGTG ACGTGGTCAG CATGCACAGG AGCTCCAAGG GTCAGGCCG TCATCACATC 1020
 CTCAGTGCCG GCCCTCACGC CCTCACCAG GCCCTGGCTA ATGGGCCCGA GGCTTAG 1077

20 (187) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 358 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: not relevant

25

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

Met Pro Ser Val Ser Pro Ala Gly Pro Ser Ala Gly Ala Val Pro Asn
 1 5 10 15
 Ala Thr Ala Val Thr Thr Val Arg Thr Asn Ala Ser Gly Leu Glu Val
 20 25 30

30

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Pro Leu Phe His Leu Phe Ala Arg Leu Asp Glu Glu Leu His Gly Thr
 35 40 45
 Phe Pro Gly Leu Cys Val Ala Leu Met Ala Val His Gly Ala Ile Phe
 50 55 60
 5 Leu Ala Gly Leu Val Leu Asn Gly Leu Ala Leu Tyr Val Phe Cys Cys
 65 70 75 80
 Arg Thr Arg Ala Lys Thr Pro Ser Val Ile Tyr Thr Ile Asn Leu Val
 85 90 95
 10 Val Thr Asp Leu Leu Val Gly Leu Ser Leu Pro Thr Arg Phe Ala Val
 100 105 110
 Tyr Tyr Gly Ala Arg Gly Cys Leu Arg Cys Ala Phe Pro His Val Leu
 115 120 125
 Gly Tyr Phe Leu Asn Met His Cys Ser Ile Leu Phe Leu Thr Cys Ile
 130 135 140
 15 Cys Val Asp Arg Tyr Leu Ala Ile Val Arg Pro Glu Gly Ser Arg Ala
 145 150 155 160
 Cys Arg Gln Pro Ala Cys Ala Arg Ala Val Cys Ala Phe Val Trp Leu
 165 170 175
 20 Ala Ala Gly Ala Val Thr Leu Ser Val Leu Gly Val Thr Gly Ser Arg
 180 185 190
 Pro Cys Cys Arg Val Phe Ala Leu Thr Val Leu Glu Phe Leu Leu Pro
 195 200 205
 Leu Leu Val Ile Ser Val Phe Thr Gly Arg Ile Met Cys Ala Leu Ser
 210 215 220
 25 Arg Pro Gly Leu Leu His Gln Gly Arg Gln Arg Arg Val Arg Ala Lys
 225 230 235 240
 Gln Leu Leu Leu Thr Val Leu Ile Ile Phe Leu Val Cys Phe Thr Pro
 245 250 255
 30 Phe His Ala Arg Gln Val Ala Val Ala Leu Trp Pro Asp Met Pro His
 260 265 270
 His Thr Ser Leu Val Val Tyr His Val Ala Val Thr Leu Ser Ser Leu
 275 280 285
 Asn Ser Cys Met Asp Pro Ile Val Tyr Cys Phe Val Thr Ser Gly Phe
 290 295 300
 35 Gln Ala Thr Val Arg Gly Leu Phe Gly Gln His Gly Glu Arg Glu Pro
 305 310 315 320
 Ser Ser Gly Asp Val Val Ser Met His Arg Ser Ser Lys Gly Ser Gly

139

325

330

335

Arg His His Ile Leu Ser Ala Gly Pro His Ala Leu Thr Gln Ala Leu
 340 345 350

Ala Asn Gly Pro Glu Ala
 355

5

(188) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1050 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

ATGAACTCCA CCTGGATGG TAATCAGAGC AGCCACCCTT TTTGCCTCTT GGCATTTGGC 60
 15 TATTTGGAAA CTGTCAATTT TTGCCTTTTG GAAGTATTGA TTATTGTCTT TCTAACTGTA 120
 TTGATTATTT CTGGCAACAT CATTGTGATT TTTGTATTTT ACTGTGCACC TTTGTTGAAC 180
 CATCACACTA CAAGTTATTT TATCCAGACT ATGGCATATG CTGACCTTTT TGTGTTGGGTG 240
 AGCTGCGTGG TCCCTTCTTT ATCACTCCTC CATCACCCCC TTCCAGTAGA GGAGTCCTTG 300
 ACTTGCCAGA TATTTGGTTT TGTAGTATCA GTTCTGAAGA GCGTCTCCAT GGCTTCTCTG 360
 20 GCCTGTATCA GCATTGATAG ATACATTGCC ATTACTAAAC CTTTAACCTA TAATACTCTG 420
 GTTACACCCT GGAGACTACG CCTGTGTATT TTCCTGATTT GGCTATACTC GACCCTGGTC 480
 TTCCTGCCTT CCTTTTCCA CTGGGGCAAA CCTGGATATC ATGGAGATGT GTTTCAGTGG 540
 TGTGCGGAGT CCTGGCACAC CGACTCCTAC TTCACCCTGT TCATCGTGAT GATGTTATAT 600
 GCCCCAGCAG CCCTTATTGT CTGCTTCACC TATTTCAACA TCTTCCGCAT CTGCCAACAG 660
 25 CACACAAAGG ATATCAGCGA AAGGCAAGCC CGCTTCAGCA GCCAGAGTGG GGAGACTGGG 720
 GAAGTGCAGG CCTGTCCTGA TAAGCGCTAT AAAATGGTCC TGTTTCGAAT CACTAGTGTA 780
 TTTTACATCC TCTGGTTGCC ATATATCATC TACTTCTTGT TGGAAAGCTC CACTGGCCAC 840
 AGCAACCGCT TCGCATCCTT CTTGACCACC TGGCTTGCTA TTAGTAACAG TTTCTGCAAC 900
 TGTGTAATTT ATAGTCTCTC CAACAGTGTA TTCCAAAGAG GACTAAAGCG CCTCTCAGGG 960
 30 GCTATGTGTA CTTCTGTGC AAGTCAGACT ACAGCCAACG ACCCTTACAC AGTTAGAAGC 1020
 AAAGGCCCTC TTAATGGATG TCATATCTGA 1050

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(189) INFORMATION FOR SEQ ID NO:188:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 349 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

5 Met Asn Ser Thr Leu Asp Gly Asn Gln Ser Ser His Pro Phe Cys Leu
 1 5 10 15
 10 Leu Ala Phe Gly Tyr Leu Glu Thr Val Asn Phe Cys Leu Leu Glu Val
 20 25 30
 Leu Ile Ile Val Phe Leu Thr Val Leu Ile Ile Ser Gly Asn Ile Ile
 35 40 45
 15 Val Ile Phe Val Phe His Cys Ala Pro Leu Leu Asn His His Thr Thr
 50 55 60
 Ser Tyr Phe Ile Gln Thr Met Ala Tyr Ala Asp Leu Phe Val Gly Val
 65 70 75 80
 20 Ser Cys Val Val Pro Ser Leu Ser Leu Leu His His Pro Leu Pro Val
 85 90 95
 Glu Glu Ser Leu Thr Cys Gln Ile Phe Gly Phe Val Val Ser Val Leu
 100 105 110
 Lys Ser Val Ser Met Ala Ser Leu Ala Cys Ile Ser Ile Asp Arg Tyr
 115 120 125
 25 Ile Ala Ile Thr Lys Pro Leu Thr Tyr Asn Thr Leu Val Thr Pro Trp
 130 135 140
 Arg Leu Arg Leu Cys Ile Phe Leu Ile Trp Leu Tyr Ser Thr Leu Val
 145 150 155 160
 30 Phe Leu Pro Ser Phe Phe His Trp Gly Lys Pro Gly Tyr His Gly Asp
 165 170 175
 Val Phe Gln Trp Cys Ala Glu Ser Trp His Thr Asp Ser Tyr Phe Thr
 180 185 190
 Leu Phe Ile Val Met Met Leu Tyr Ala Pro Ala Ala Leu Ile Val Cys
 195 200 205
 35 Phe Thr Tyr Phe Asn Ile Phe Arg Ile Cys Gln Gln His Thr Lys Asp
 210 215 220

141

Ile Ser Glu Arg Gln Ala Arg Phe Ser Ser Gln Ser Gly Glu Thr Gly
 225 230 235 240

Glu Val Gln Ala Cys Pro Asp Lys Arg Tyr Lys Met Val Leu Phe Arg
 245 250 255

5 Ile Thr Ser Val Phe Tyr Ile Leu Trp Leu Pro Tyr Ile Ile Tyr Phe
 260 265 270

Leu Leu Glu Ser Ser Thr Gly His Ser Asn Arg Phe Ala Ser Phe Leu
 275 280 285

10 Thr Thr Trp Leu Ala Ile Ser Asn Ser Phe Cys Asn Cys Val Ile Tyr
 290 295 300

Ser Leu Ser Asn Ser Val Phe Gln Arg Gly Leu Lys Arg Leu Ser Gly
 305 310 315 320

Ala Met Cys Thr Ser Cys Ala Ser Gln Thr Thr Ala Asn Asp Pro Tyr
 325 330 335

15 Thr Val Arg Ser Lys Gly Pro Leu Asn Gly Cys His Ile
 340 345

(190) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1302 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

25 ATGTGTTTTT CTCCCATCTT GGAAATCAAC ATGCAGTCTG AATCTAACAT TACAGTGC GA 60
 GATGACATTG ATGACATCAA CACCAATATG TACCAACCAC TATCATATCC GTTAAGCTTT 120
 CAAGTGTCTC TCACCGGATT TCTTATGTGA GAAATTGTGT TGGGACTTGG CAGCAACCTC 180
 ACTGTATTGG TACTTTACTG CATGAAATCC AACTTAATCA ACTCTGTCAG TAACATTATT 240
 ACAATGAATC TTCATGTACT TGATGTAATA ATTTGTGTGG GATGTATTCC TCTAACTATA 300
 30 GTTATCCTTC TGCTTTCCTT GGAGAGTAAC ACTGCTCTCA TTTGCTGTTT CCATGAGGCT 360
 TGTGTATCTT TTGCAAGTGT CTCAACAGCA ATCAACGTTT TTGCTATCAC TTTGGACAGA 420
 TATGACATCT CTGTAAAACC TGCAAACCGA ATTCTGACAA TGGGCAGAGC TGTAATGTTA 480
 ATGATATCCA TTTGGATTTT TTCTTTTTC TCTTTCCTGA TTCCTTTTAT TGAGGTAAAT 540
 TTTTTCAGTC TTCAAAGTGG AAATACCTGG GAAAACAAGA CACTTTTATG TGTCAGTACA 600

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AATGAATACT ACACTGAACT GGAATGTAT TATCACCTGT TAGTACAGAT CCCAATATTC 660
 TTTTTCCTG TTGTAGTAAT GTTAATCACA TACACCAAAA TACTTCAGGC TCTTAATATT 720
 CGAATAGGCA CAAGATTTTC AACAGGGCAG AAGAAGAAAG CAAGAAAGAA AAAGACAATT 780
 TCTCTAACCA CACAACATGA GGCTACAGAC ATGTCACAAA GCAGTGGTGG GAGAAATGTA 840
 5 GTCTTTGGTG TAAGAACTTC AGTTTCTGTA ATAATTGCCC TCCGGCGAGC TGTGAAACGA 900
 CACCGTGAAC GACGAGAAAG ACAAAGAGA GTCAAGAGGA TGTCTTTATT GATTATTTCT 960
 ACATTTCTTC TCTGCTGGAC ACCAATTTCT GTTTTAAATA CCACCATTTT ATGTTTAGGC 1020
 CCAAGTGACC TTTTAGTAAA ATTAAGATTG TGTTTTTTAG TCATGGCTTA TGGAACAACT 1080
 ATATTTCACT CTCTATTATA TGCATTCCT AGACAAAAAT TTCAAAGGT CTTGAAAAGT 1140
 10 AAAATGAAAA AGCGAGTTGT TTCTATAGTA GAAGCTGATC CCCTGCCTAA TAATGCTGTA 1200
 ATACACAACCT CTTGGATAGA TCCCAAAAGA AACAAAAAAA TTACCTTTGA AGATAGTGAA 1260
 ATAAGAGAAA AACGTTTAGT GCCTCAGGTT GTCACAGACT AG 1302

(191) INFORMATION FOR SEQ ID NO:190:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 433 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

- 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

Met Cys Phe Ser Pro Ile Leu Glu Ile Asn Met Gln Ser Glu Ser Asn
 1 5 10 15

Ile Thr Val Arg Asp Asp Ile Asp Asp Ile Asn Thr Asn Met Tyr Gln
 20 25 30

- 25 Pro Leu Ser Tyr Pro Leu Ser Phe Gln Val Ser Leu Thr Gly Phe Leu
 35 40 45

Met Leu Glu Ile Val Leu Gly Leu Gly Ser Asn Leu Thr Val Leu Val
 50 55 60

- 30 Leu Tyr Cys Met Lys Ser Asn Leu Ile Asn Ser Val Ser Asn Ile Ile
 65 70 75 80

Thr Met Asn Leu His Val Leu Asp Val Ile Ile Cys Val Gly Cys Ile
 85 90 95

Pro Leu Thr Ile Val Ile Leu Leu Leu Ser Leu Glu Ser Asn Thr Ala

143

	100	105	110
	Leu Ile Cys Cys Phe His Glu Ala Cys Val Ser Phe Ala Ser Val Ser		
	115	120	125
5	Thr Ala Ile Asn Val Phe Ala Ile Thr Leu Asp Arg Tyr Asp Ile Ser		
	130	135	140
	Val Lys Pro Ala Asn Arg Ile Leu Thr Met Gly Arg Ala Val Met Leu		
	145	150	155
	Met Ile Ser Ile Trp Ile Phe Ser Phe Phe Ser Phe Leu Ile Pro Phe		
	165	170	175
10	Ile Glu Val Asn Phe Phe Ser Leu Gln Ser Gly Asn Thr Trp Glu Asn		
	180	185	190
	Lys Thr Leu Leu Cys Val Ser Thr Asn Glu Tyr Tyr Thr Glu Leu Gly		
	195	200	205
15	Met Tyr Tyr His Leu Leu Val Gln Ile Pro Ile Phe Phe Phe Thr Val		
	210	215	220
	Val Val Met Leu Ile Thr Tyr Thr Lys Ile Leu Gln Ala Leu Asn Ile		
	225	230	235
	Arg Ile Gly Thr Arg Phe Ser Thr Gly Gln Lys Lys Lys Ala Arg Lys		
	245	250	255
20	Lys Lys Thr Ile Ser Leu Thr Thr Gln His Glu Ala Thr Asp Met Ser		
	260	265	270
	Gln Ser Ser Gly Gly Arg Asn Val Val Phe Gly Val Arg Thr Ser Val		
	275	280	285
25	Ser Val Ile Ile Ala Leu Arg Arg Ala Val Lys Arg His Arg Glu Arg		
	290	295	300
	Arg Glu Arg Gln Lys Arg Val Lys Arg Met Ser Leu Leu Ile Ile Ser		
	305	310	315
	Thr Phe Leu Leu Cys Trp Thr Pro Ile Ser Val Leu Asn Thr Thr Ile		
	325	330	335
30	Leu Cys Leu Gly Pro Ser Asp Leu Leu Val Lys Leu Arg Leu Cys Phe		
	340	345	350
	Leu Val Met Ala Tyr Gly Thr Thr Ile Phe His Pro Leu Leu Tyr Ala		
	355	360	365
35	Phe Thr Arg Gln Lys Phe Gln Lys Val Leu Lys Ser Lys Met Lys Lys		
	370	375	380
	Arg Val Val Ser Ile Val Glu Ala Asp Pro Leu Pro Asn Asn Ala Val		
	385	390	395
			400

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Ile His Asn Ser Trp Ile Asp Pro Lys Arg Asn Lys Lys Ile Thr Phe
405 410 415

Glu Asp Ser Glu Ile Arg Glu Lys Arg Leu Val Pro Gln Val Val Thr
420 425 430

5 Asp

(192) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1209 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

15 ATGTTGTGTC CTTCCAAGAC AGATGGCTCA GGGCACTCTG GTAGGATTCA CCAGGAAACT 60
CATGGAGAAG GGAAAAGGGA CAAGATTAGC AACAGTGAAG GGAGGCAGAA TGGTGGGAGA 120
GGATTCCAGA TGAACGGTGG GTCGCTGGAG GCTGAGCATG CCAGCAGGAT GTCAGTTCTC 180
AGAGCAAAGC CCATGTCAAA CAGCCAACGC TTGCTCCTTC TGTCCCCAGG ATCACCTCTT 240
CGCACGGGGA GCATCTCCTA CATCAACATC ATCATGCCTT CGGTGTTCGG CACCATCTGC 300
20 CTCCTGGGCA TCATCGGGAA CTCCACGGTC ATCTTCGGG TCGTGAAGAA GTCCAAGCTG 360
CACTGGTGCA ACAACGTCCC CGACATCTTC ATCATCAACC TCTCGGTAGT AGATCTCCTC 420
TTTCTCCTGG GCATGCCCTT CATGATCCAC CAGCTCATGG GCAATGGGGT GTGGCACTTT 480
GGGGAGACCA TGTGCACCCT CATCACGGCC ATGGATGCCA ATAGTCAGTT CACCAGCACC 540
TACATCCTGA CCGCCATGGC CATTGACCGC TACCTGGCCA CTGTCCACCC CATCTCTTCC 600
25 ACGAAGTTCC GGAAGCCCTC TGTGGCCACC CTGGTGATCT GCCTCCTGTG GGCCCTCTCC 660
TTCATCAGCA TCACCCCTGT GTGGCTGTAT GCCAGACTCA TCCCCTTCCC AGGAGGTGCA 720
GTGGGCTGCG GCATACGCCT GCCCAACCCA GACACTGACC TCTACTGGTT CACCCTGTAC 780
CAGTTTTTCC TGGCCTTTGC CCTGCCTTTT GTGGTCATCA CAGCCGCATA CGTGAGGATC 840
CTGCAGCGCA TGACGTCCTC AGTGGCCCCC GCCTCCCAGC GCAGCATCCG GCTGCGGACA 900
30 AAGAGGGTGA AACGCACAGC CATCGCCATC TGTCTGGTCT TCTTTGTGTG CTGGGCACCC 960
TACTATGTGC TACAGCTGAC CCAGTTGTCC ATCAGCCGCC CGACCCTCAC CTTTGTCTAC 1020
TTATACAATG CGGCCATCAG CTTGGGCTAT GCCAACAGCT GCCTCAACCC CTTTGTGTAC 1080

145

ATCGTGCTCT GTGAGACGTT CCGCAAACGC TTGGTCCTGT CGGTGAAGCC TGCAGCCCAG 1140
 GGGCAGCTTC GCGCTGTCAG CAACGCTCAG ACGGCTGACG AGGAGAGGAC AGAAAGCAAA 1200
 GGCACCTCA 1209

(193) INFORMATION FOR SEQ ID NO:192:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 402 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

- 10 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

Met Leu Cys Pro Ser Lys Thr Asp Gly Ser Gly His Ser Gly Arg Ile
 1 5 10 15
 His Gln Glu Thr His Gly Glu Gly Lys Arg Asp Lys Ile Ser Asn Ser
 20 25 30
 Glu Gly Arg Glu Asn Gly Gly Arg Gly Phe Gln Met Asn Gly Gly Ser
 35 40 45
 Leu Glu Ala Glu His Ala Ser Arg Met Ser Val Leu Arg Ala Lys Pro
 50 55 60
 Met Ser Asn Ser Gln Arg Leu Leu Leu Leu Ser Pro Gly Ser Pro Pro
 65 70 75 80
 Arg Thr Gly Ser Ile Ser Tyr Ile Asn Ile Ile Met Pro Ser Val Phe
 85 90 95
 Gly Thr Ile Cys Leu Leu Gly Ile Ile Gly Asn Ser Thr Val Ile Phe
 100 105 110
 Ala Val Val Lys Lys Ser Lys Leu His Trp Cys Asn Asn Val Pro Asp
 115 120 125
 Ile Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu Phe Leu Leu Gly
 130 135 140
 Met Pro Phe Met Ile His Gln Leu Met Gly Asn Gly Val Trp His Phe
 145 150 155 160
 Gly Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp Ala Asn Ser Gln
 165 170 175
 Phe Thr Ser Thr Tyr Ile Leu Thr Ala Met Ala Ile Asp Arg Tyr Leu
 180 185 190
 Ala Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg Lys Pro Ser Val

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	195	200	205
	Ala Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser Phe Ile Ser Ile		
	210	215	220
5	Thr Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe Pro Gly Gly Ala		
	225	230	235 240
	Val Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr Asp Leu Tyr Trp		
		245	250 255
	Phe Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu Pro Phe Val Val		
		260	265 270
10	Ile Thr Ala Ala Tyr Val Arg Ile Leu Gln Arg Met Thr Ser Ser Val		
		275	280 285
	Ala Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr Lys Arg Val Lys		
		290	295 300
15	Arg Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val Cys Trp Ala Pro		
		305	310 315 320
	Tyr Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser Arg Pro Thr Leu		
		325	330 335
	Thr Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu Gly Tyr Ala Asn		
		340	345 350
20	Ser Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys Glu Thr Phe Arg		
		355	360 365
	Lys Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln Gly Gln Leu Arg		
		370	375 380
25	Ala Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg Thr Glu Ser Lys		
		385	390 395 400
	Gly Thr		

(194) INFORMATION FOR SEQ ID NO:193:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1128 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

ATGGATGTGA CTTCCCAAGC CCGGGGCGTG GGCCTGGAGA TGTACCCAGG CACCGCGCAC 60
 GCTGCGGCCC CCAACACCAC CTCCCCGAG CTCAACCTGT CCCACCGCT CCTGGGCACC 120

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GCCCTGGCCA ATGGGACAGG TGAGCTCTCG GAGCACCAGC AGTACGTGAT CGGCCTGTTC 180
 CTCTCGTGCC TCTACACCAT CTTCTCTTC CCCATCGGCT TTGTGGGCAA CATCCTGATC 240
 CTGGTGGTGA ACATCAGCTT CCGCGAGAAG ATGACCATCC CCGACCTGTA CTTCATCAAC 300
 CTGGCGGTGG CGGACCTCAT CCTGGTGGCC GACTCCCTCA TTGAGGTGTT CAACCTGCAC 360
 5 GAGCGGTACT ACGACATCGC CGTCCTGTGC ACCTTCATGT CGCTCTTCCT GCAGGTCAAC 420
 ATGTACAGCA GCGTCTTCTT CCTCACCTGG ATGAGCTTCG ACCGCTACAT CGCCCTGGCC 480
 AGGGCCATGC GCTGCAGCCT GTTCCGCACC AAGCACCACG CCCGGCTGAG CTGTGGCCTC 540
 ATCTGGATGG CATCCGTGTC AGCCACGCTG GTGCCCTTCA CCGCCGTGCA CCTGCAGCAC 600
 ACCGACGAGG CCTGCTTCTG TTTCGCGGAT GTCCGGGAGG TGCAGTGGCT CGAGGTCACG 660
 10 CTGGGCTTCA TCGTGCCCTT CGCCATCATC GGCCTGTGCT ACTCCCTCAT TGTCCGGGTG 720
 CTGGTCAGGG CGCACCAGCA CCGTGGGCTG CGGCCCCGGC GGCAGAAGGC GAAACGCATG 780
 ATCCTCGCGG TGGTGCTGGT CTTCTTCGTC TGCTGGCTGC CGGAGAACGT CTTCATCAGC 840
 GTGCACCTCC TGCAGCGGAC GCAGCCTGGG GCCGCTCCCT GCAAGCAGTC TTTCCGCCAT 900
 GCCCACCCCC TCACGGGCCA CATTGTCAAC CTCGCCGCCT TCTCCAACAG CTGCCTAAAC 960
 15 CCCCTCATCT ACAGCTTCTT CGGGGAGACC TTCAGGGACA AGCTGAGGCT GTACATTGAG 1020
 CAGAAAACAA ATTTGCCGGC CCTGAACCGC TTCTGTCACG CTGCCCTGAA GGCCGTCATT 1080
 CCAGACAGCA CCGAGCAGTC GGATGTGAGG TTCAGCAGTG CCGTGTGA 1128

(195) INFORMATION FOR SEQ ID NO:194:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 375 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

Met Asp Val Thr Ser Gln Ala Arg Gly Val Gly Leu Glu Met Tyr Pro
 1 5 10 15

Gly Thr Ala His Ala Ala Ala Pro Asn Thr Thr Ser Pro Glu Leu Asn
 20 25 30

30 Leu Ser His Pro Leu Leu Gly Thr Ala Leu Ala Asn Gly Thr Gly Glu
 35 40 45

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Leu Ser Glu His Gln Gln Tyr Val Ile Gly Leu Phe Leu Ser Cys Leu
 50 55 60

Tyr Thr Ile Phe Leu Phe Pro Ile Gly Phe Val Gly Asn Ile Leu Ile
 65 70 75 80

5 Leu Val Val Asn Ile Ser Phe Arg Glu Lys Met Thr Ile Pro Asp Leu
 85 90 95

Tyr Phe Ile Asn Leu Ala Val Ala Asp Leu Ile Leu Val Ala Asp Ser
 100 105 110

10 Leu Ile Glu Val Phe Asn Leu His Glu Arg Tyr Tyr Asp Ile Ala Val
 115 120 125

Leu Cys Thr Phe Met Ser Leu Phe Leu Gln Val Asn Met Tyr Ser Ser
 130 135 140

Val Phe Phe Leu Thr Trp Met Ser Phe Asp Arg Tyr Ile Ala Leu Ala
 145 150 155 160

15 Arg Ala Met Arg Cys Ser Leu Phe Arg Thr Lys His His Ala Arg Leu
 165 170 175

Ser Cys Gly Leu Ile Trp Met Ala Ser Val Ser Ala Thr Leu Val Pro
 180 185 190

Phe Thr Ala Val His Leu Gln His Thr Asp Glu Ala Cys Phe Cys Phe
 195 200 205

20 Ala Asp Val Arg Glu Val Gln Trp Leu Glu Val Thr Leu Gly Phe Ile
 210 215 220

Val Pro Phe Ala Ile Ile Gly Leu Cys Tyr Ser Leu Ile Val Arg Val
 225 230 235 240

25 Leu Val Arg Ala His Arg His Arg Gly Leu Arg Pro Arg Arg Gln Lys
 245 250 255

Ala Lys Arg Met Ile Leu Ala Val Val Leu Val Phe Phe Val Cys Trp
 260 265 270

Leu Pro Glu Asn Val Phe Ile Ser Val His Leu Leu Gln Arg Thr Gln
 275 280 285

30 Pro Gly Ala Ala Pro Cys Lys Gln Ser Phe Arg His Ala His Pro Leu
 290 295 300

Thr Gly His Ile Val Asn Leu Ala Ala Phe Ser Asn Ser Cys Leu Asn
 305 310 315 320

35 Pro Leu Ile Tyr Ser Phe Leu Gly Glu Thr Phe Arg Asp Lys Leu Arg
 325 330 335

Leu Tyr Ile Glu Gln Lys Thr Asn Leu Pro Ala Leu Asn Arg Phe Cys

149

340

345

350

His Ala Ala Leu Lys Ala Val Ile Pro Asp Ser Thr Glu Gln Ser Asp
 355 360 365

Val Arg Phe Ser Ser Ala Val
 370 375

5.

(196) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 960 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

ATGCCATTCC CAAACTGCTC AGCCCCCAGC ACTGTGGTGG CCACAGCTGT GGGTGTCTTG 60
 15 CTGGGGCTGG AGTGTGGGCT GGGTCTGCTG GGCAACGCGG TGGCGCTGTG GACCTTCCTG 120
 TTCCGGGTCA GGGTGTGGAA GCCGTACGCT GTCTACCTGC TCAACCTGGC CCTGGCTGAC 180
 CTGCTGTTGG CTGCGTGCCT GCCTTTCCTG GCCGCCTTCT ACCTGAGCCT CCAGGCTTGG 240
 CATCTGGGCC GTGTGGGCTG CTGGGCCCTG CGCTTCCTGC TGGACCTCAG CCGCAGCGTG 300
 GGGATGGCCT TCCTGGCCGC CGTGGCTTTG GACCGGTACC TCCGTGTGGT CCACCCCTCGG 360
 20 CTTAAGGTCA ACCTGCTGTC TCCTCAGGCG GCCCTGGGGG TCTCGGGCCT CGTCTGGCTC 420
 CTGATGGTGC CCCTCACCTG CCCGGGCTTG CTCATCTCTG AGGCCGCCCA GAACTCCACC 480
 AGGTGCCACA GTTCTACTC CAGGGCAGAC GGCTCCTTCA GCATCATCTG GCAGGAAGCA 540
 CTCTCCTGCC TTCAGTTTGT CCTCCCCTTT GGCCTCATCG TGTTCTGCAA TGCAGGCATC 600
 ATCAGGGCTC TCCAGAAAAG ACTCCGGGAG CCTGAGAAAC AGCCCAAGCT TCAGCGGGCC 660
 25 AAGGCACTGG TCACCTTGGT GGTGGTGTG TTTGCTCTGT GCTTTCTGCC CTGCTTCCTG 720
 GCCAGAGTCC TGATGCACAT CTTCCAGAAT CTGGGGAGCT GCAGGGCCCT TTGTGCAGTG 780
 GCTCATACCT CGGATGTCAC GGGCAGCCTC ACCTACCTGC ACAGTGTCTG CAACCCCGTG 840
 GTATACTGCT TCTCCAGCCC CACCTTCAGG AGCTCCTATC GGAGGGTCTT CCACACCCTC 900
 CGAGGCAAAG GGCAGGCAGC AGAGCCCCCA GATTTCAACC CCAGAGACTC CTATTCCTGA 960

30 (197) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

150

- (A) LENGTH: 319 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

5 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

	Met	Pro	Phe	Pro	Asn	Cys	Ser	Ala	Pro	Ser	Thr	Val	Val	Ala	Thr	Ala	1	5	10	15
10	Val	Gly	Val	Leu	Leu	Gly	Leu	Glu	Cys	Gly	Leu	Gly	Leu	Leu	Gly	Asn	20	25	30	
	Ala	Val	Ala	Leu	Trp	Thr	Phe	Leu	Phe	Arg	Val	Arg	Val	Trp	Lys	Pro	35	40	45	
	Tyr	Ala	Val	Tyr	Leu	Leu	Asn	Leu	Ala	Leu	Ala	Asp	Leu	Leu	Leu	Ala	50	55	60	
15	Ala	Cys	Leu	Pro	Phe	Leu	Ala	Ala	Phe	Tyr	Leu	Ser	Leu	Gln	Ala	Trp	65	70	75	80
	His	Leu	Gly	Arg	Val	Gly	Cys	Trp	Ala	Leu	Arg	Phe	Leu	Leu	Asp	Leu	85	90	95	
20	Ser	Arg	Ser	Val	Gly	Met	Ala	Phe	Leu	Ala	Ala	Val	Ala	Leu	Asp	Arg	100	105	110	
	Tyr	Leu	Arg	Val	Val	His	Pro	Arg	Leu	Lys	Val	Asn	Leu	Leu	Ser	Pro	115	120	125	
	Gln	Ala	Ala	Leu	Gly	Val	Ser	Gly	Leu	Val	Trp	Leu	Leu	Met	Val	Ala	130	135	140	
25	Leu	Thr	Cys	Pro	Gly	Leu	Leu	Ile	Ser	Glu	Ala	Ala	Gln	Asn	Ser	Thr	145	150	155	160
	Arg	Cys	His	Ser	Phe	Tyr	Ser	Arg	Ala	Asp	Gly	Ser	Phe	Ser	Ile	Ile	165	170	175	
30	Trp	Gln	Glu	Ala	Leu	Ser	Cys	Leu	Gln	Phe	Val	Leu	Pro	Phe	Gly	Leu	180	185	190	
	Ile	Val	Phe	Cys	Asn	Ala	Gly	Ile	Ile	Arg	Ala	Leu	Gln	Lys	Arg	Leu	195	200	205	
	Arg	Glu	Pro	Glu	Lys	Gln	Pro	Lys	Leu	Gln	Arg	Ala	Lys	Ala	Leu	Val	210	215	220	
35	Thr	Leu	Val	Val	Val	Leu	Phe	Ala	Leu	Cys	Phe	Leu	Pro	Cys	Phe	Leu	225	230	235	240
	Ala	Arg	Val	Leu	Met	His	Ile	Phe	Gln	Asn	Leu	Gly	Ser	Cys	Arg	Ala				

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		245		250		255	
	Leu Cys Ala Val Ala His Thr Ser Asp Val Thr Gly Ser Leu Thr Tyr						
		260		265		270	
5	Leu His Ser Val Val Asn Pro Val Val Tyr Cys Phe Ser Ser Pro Thr						
		275		280		285	
	Phe Arg Ser Ser Tyr Arg Arg Val Phe His Thr Leu Arg Gly Lys Gly						
		290		295		300	
	Gln Ala Ala Glu Pro Pro Asp Phe Asn Pro Arg Asp Ser Tyr Ser						
		305		310		315	
10	(198) INFORMATION FOR SEQ ID NO:197:						
	(i) SEQUENCE CHARACTERISTICS:						
	(A) LENGTH: 1143 base pairs						
	(B) TYPE: nucleic acid						
	(C) STRANDEDNESS: single						
15	(D) TOPOLOGY: linear						
	(ii) MOLECULE TYPE: DNA (genomic)						
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:						
	ATGGAGGAAG GTGGTGATTT TGACAACTAC TATGGGGCAG ACAACCAGTC TGAGTGTGAG					60	
	TACACAGACT GGAAATCCTC GGGGGCCCTC ATCCCTGCCA TCTACATGTT GGTCTTCCTC					120	
20	CTGGGCACCA CGGGAAACGG TCTGGTGCTC TGGACCGTGT TTCGGAGCAG CCGGGAGAAG					180	
	AGGCGCTCAG CTGATATCTT CATTGCTAGC CTGGCGGTGG CTGACCTGAC CTTCTGTGGT					240	
	ACGCTGCCCC TGTGGGCTAC CTACACGTAC CGGGACTATG ACTGGCCCTT TGGGACCTTC					300	
	TTCTGCAAGC TCAGCAGCTA CCTCATCTTC GTCAACATGT ACGCCAGCGT CTTCTGCCTC					360	
	ACCGGCCTCA GCTTCGACCG CTACCTGGCC ATCGTGAGGC CAGTGGCCAA TGCTCGGCTG					420	
25	AGGCTGCGGG TCAGCGGGGC CGTGGCCACG GCAGTTCTTT GGGTGCTGGC CGCCCTCCTG					480	
	GCCATGCCTG TCATGGTGTT ACGCACCACC GGGGACTTGG AGAACACCAC TAAGGTGCAG					540	
	TGCTACATGG ACTACTCCAT GGTGGCCACT GTGAGCTCAG AGTGGGCCTG GGAGGTGGGC					600	
	CTTGGGGTCT CGTCCACCAC CGTGGGCTTT GTGGTGCCCT TCACCATCAT GCTGACCTGT					660	
	TACTTCTTCA TCGCCCAAAC CATCGCTGGC CACTTCCGCA AGGAACGCAT CGAGGGCCTG					720	
30	CGGAAGCGGC GCCGGCTTAA GAGCATCATC GTGGTGCTGG TGGTGACCTT TGCCCTGTGC					780	
	TGGATGCCCT ACCACCTGGT GAAGACGCTG TACATGCTGG GCAGCCTGCT GCACTGGCCC					840	
	TGTGACTTTG ACCTCTTCCT CATGAACATC TTCCCCTACT GCACCTGCAT CAGCTACGTC					900	

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AACAGCTGCC TCAACCCCTT CCTCTATGCC TTTTTCGACC CCCGCTTCCG CCAGGCCTGC 960
 ACCTCCATGC TCTGCTGTGG CCAGAGCAGG TGCGCAGGCA CCTCCCACAG CAGCAGTGGG 1020
 GAGAAGTCAG CCAGCTACTC TTCGGGGCAC AGCCAGGGGC CCGGCCCCAA CATCGGCAAG 1080
 GGTGGAGAAC AGATGCACGA GAAATCCATC CCCTACAGCC AGGAGACCCT TGTGGTTGAC 1140
 5 TAG 1143

(199) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 380 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant
 (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

10 Met Glu Glu Gly Gly Asp Phe Asp Asn Tyr Tyr Gly Ala Asp Asn Gln
 1 5 10 15
 Ser Glu Cys Glu Tyr Thr Asp Trp Lys Ser Ser Gly Ala Leu Ile Pro
 20 25 30
 Ala Ile Tyr Met Leu Val Phe Leu Leu Gly Thr Thr Gly Asn Gly Leu
 35 40 45
 20 Val Leu Trp Thr Val Phe Arg Ser Ser Arg Glu Lys Arg Arg Ser Ala
 50 55 60
 Asp Ile Phe Ile Ala Ser Leu Ala Val Ala Asp Leu Thr Phe Val Val
 65 70 75 80
 25 Thr Leu Pro Leu Trp Ala Thr Tyr Thr Tyr Arg Asp Tyr Asp Trp Pro
 85 90 95
 Phe Gly Thr Phe Phe Cys Lys Leu Ser Ser Tyr Leu Ile Phe Val Asn
 100 105 110
 Met Tyr Ala Ser Val Phe Cys Leu Thr Gly Leu Ser Phe Asp Arg Tyr
 115 120 125
 30 Leu Ala Ile Val Arg Pro Val Ala Asn Ala Arg Leu Arg Leu Arg Val
 130 135 140
 Ser Gly Ala Val Ala Thr Ala Val Leu Trp Val Leu Ala Ala Leu Leu
 145 150 155 160
 35 Ala Met Pro Val Met Val Leu Arg Thr Thr Gly Asp Leu Glu Asn Thr
 165 170 175

153

Thr Lys Val Gln Cys Tyr Met Asp Tyr Ser Met Val Ala Thr Val Ser
 180 185 190
 Ser Glu Trp Ala Trp Glu Val Gly Leu Gly Val Ser Ser Thr Thr Val
 195 200 205
 5 Gly Phe Val Val Pro Phe Thr Ile Met Leu Thr Cys Tyr Phe Phe Ile
 210 215 220
 Ala Gln Thr Ile Ala Gly His Phe Arg Lys Glu Arg Ile Glu Gly Leu
 225 230 235 240
 10 Arg Lys Arg Arg Arg Leu Lys Ser Ile Ile Val Val Leu Val Val Thr
 245 250 255
 Phe Ala Leu Cys Trp Met Pro Tyr His Leu Val Lys Thr Leu Tyr Met
 260 265 270
 Leu Gly Ser Leu Leu His Trp Pro Cys Asp Phe Asp Leu Phe Leu Met
 275 280 285
 15 Asn Ile Phe Pro Tyr Cys Thr Cys Ile Ser Tyr Val Asn Ser Cys Leu
 290 295 300
 Asn Pro Phe Leu Tyr Ala Phe Phe Asp Pro Arg Phe Arg Gln Ala Cys
 305 310 315 320
 20 Thr Ser Met Leu Cys Cys Gly Gln Ser Arg Cys Ala Gly Thr Ser His
 325 330 335
 Ser Ser Ser Gly Glu Lys Ser Ala Ser Tyr Ser Ser Gly His Ser Gln
 340 345 350
 Gly Pro Gly Pro Asn Met Gly Lys Gly Gly Glu Gln Met His Glu Lys
 355 360 365
 25 Ser Ile Pro Tyr Ser Gln Glu Thr Leu Val Val Asp
 370 375 380

(200) INFORMATION FOR SEQ ID NO:199:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1119 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:
 35 ATGAACTACC CGCTAACGCT GGAAATGGAC CTCGAGAACC TGGAGGACCT GTTCTGGGAA 60
 CTGGACAGAT TGGACAACTA TAACGACACC TCCCTGGTGG AAAATCATCT CTGCCCTGCC 120

ACAGAGGGTC CCCTCATGGC CTCCTTCAAG GCCGTGTTTCG TGCCCGTGGC CTACAGCCTC 180
 ATCTTCCTCC TGGGCGTGAT CGGCAACGTC CTGGTGCTGG TGATCCTGGA GCGGCACCGG 240
 CAGACACGCA GTTCCACGGA GACCTTCCTG TTCCACCTGG CCGTGGCCGA CCTCCTGCTG 300
 GTCTTCATCT TGCCCTTTGC CGTGGCCGAG GGCTCTGTGG GCTGGGTCCT GGGGACCTTC 360
 5 CTCTGCAAAA CTGTGATTGC CCTGCACAAA GTCAACTTCT ACTGCAGCAG CCTGCTCCTG 420
 GCCTGCATCG CCGTGGACCG CTACCTGGCC ATTGTCCACG CCGTCCATGC CTACCGCCAC 480
 CGCCGCCTCC TCTCCATCCA CATCACCTGT GGGACCATCT GGCTGGTGGG CTTCTCCTT 540
 GCCTTGCCAG AGATTCTCTT CGCCAAAGTC AGCCAAGGCC ATCACAACAA CTCCCTGCCA 600
 CGTTGCACCT TCTCCCAAGA GAACCAAGCA GAAACGCATG CCTGGTTCAC CTCCCGATTC 660
 10 CTCTACCATG TGGCGGGATT CCTGCTGCCC ATGCTGGTGA TGGGCTGGTG CTACGTGGGG 720
 GTAGTGACA GGTGCGCCA GGCCAGCGG CGCCCTCAGC GGCAGAAGGC AAAAAGGGTG 780
 GCCATCCTGG TGACAAGCAT CTTCTTCCTC TGCTGGTCAC CCTACCACAT CGTCATCTTC 840
 CTGGACACCC TGGCGAGGCT GAAGGCCGTG GACAATACCT GCAAGCTGAA TGGCTCTCTC 900
 CCCGTGGCCA TCACCATGTG TGAGTTCCTG GGCTGGCCC ACTGCTGCCT CAACCCCATG 960
 15 CTCTACACTT TCGCCGGCGT GAAGTTCGCG AGTGACCTGT CGCGGCTCCT GACCAAGCTG 1020
 GGCTGTACCG GCCCTGCCTC CCTGTGCCAG CTCTTCCCTA GCTGGCGCAG GAGCAGTCTC 1080
 TCTGAGTCAG AGAATGCCAC CTCTCTCACC ACGTTCTAG 1119

(201) INFORMATION FOR SEQ ID NO:200:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 372 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant
 (ii) MOLECULE TYPE: protein

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:
 Met Asn Tyr Pro Leu Thr Leu Glu Met Asp Leu Glu Asn Leu Glu Asp
 1 5 10 15
 Leu Phe Trp Glu Leu Asp Arg Leu Asp Asn Tyr Asn Asp Thr Ser Leu
 20 25 30
 30 Val Glu Asn His Leu Cys Pro Ala Thr Glu Gly Pro Leu Met Ala Ser
 35 40 45
 Phe Lys Ala Val Phe Val Pro Val Ala Tyr Ser Leu Ile Phe Leu Leu

155

	50	55	60
	Gly Val Ile Gly Asn Val Leu Val Leu Val Ile Leu Glu Arg His Arg		
	65	70	75 80
5	Gln Thr Arg Ser Ser Thr Glu Thr Phe Leu Phe His Leu Ala Val Ala		
		85	90 95
	Asp Leu Leu Leu Val Phe Ile Leu Pro Phe Ala Val Ala Glu Gly Ser		
		100	105 110
	Val Gly Trp Val Leu Gly Thr Phe Leu Cys Lys Thr Val Ile Ala Leu		
		115	120 125
10	His Lys Val Asn Phe Tyr Cys Ser Ser Leu Leu Leu Ala Cys Ile Ala		
		130	135 140
	Val Asp Arg Tyr Leu Ala Ile Val His Ala Val His Ala Tyr Arg His		
		145	150 155 160
15	Arg Arg Leu Leu Ser Ile His Ile Thr Cys Gly Thr Ile Trp Leu Val		
		165	170 175
	Gly Phe Leu Leu Ala Leu Pro Glu Ile Leu Phe Ala Lys Val Ser Gln		
		180	185 190
	Gly His His Asn Asn Ser Leu Pro Arg Cys Thr Phe Ser Gln Glu Asn		
		195	200 205
20	Gln Ala Glu Thr His Ala Trp Phe Thr Ser Arg Phe Leu Tyr His Val		
		210	215 220
	Ala Gly Phe Leu Leu Pro Met Leu Val Met Gly Trp Cys Tyr Val Gly		
		225	230 235 240
25	Val Val His Arg Leu Arg Gln Ala Gln Arg Arg Pro Gln Arg Gln Lys		
		245	250 255
	Ala Lys Arg Val Ala Ile Leu Val Thr Ser Ile Phe Phe Leu Cys Trp		
		260	265 270
	Ser Pro Tyr His Ile Val Ile Phe Leu Asp Thr Leu Ala Arg Leu Lys		
		275	280 285
30	Ala Val Asp Asn Thr Cys Lys Leu Asn Gly Ser Leu Pro Val Ala Ile		
		290	295 300
	Thr Met Cys Glu Phe Leu Gly Leu Ala His Cys Cys Leu Asn Pro Met		
		305	310 315 320
35	Leu Tyr Thr Phe Ala Gly Val Lys Phe Arg Ser Asp Leu Ser Arg Leu		
		325	330 335
	Leu Thr Lys Leu Gly Cys Thr Gly Pro Ala Ser Leu Cys Gln Leu Phe		
		340	345 350

156

Pro Ser Trp Arg Arg Ser Ser Leu Ser Glu Ser Glu Asn Ala Thr Ser
 355 360 365

Leu Thr Thr Phe
 370

5 (202) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1128 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

10 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

ATGGATGTGA CTTCCCAAGC CCGGGGCGTG GGCCTGGAGA TGTACCCAGG CACCGCGCAG 60
 CCTGCGGCCC CCAACACCAC CTCCCCGAG CTCAACCTGT CCCACCCGCT CCTGGGCACC 120
 15 GCCCTGGCCA ATGGGACAGG TGAGCTCTCG GAGCACCAGC AGTACGTGAT CGGCCTGTTC 180
 CTCTCGTGCC TCTACACCAT CTTCTCTTC CCCATCGGCT TTGTGGGCAA CATCCTGATC 240
 CTGGTGGTGA ACATCAGCTT CCGCGAGAAG ATGACCATCC CCGACCTGTA CTTTCATCAAC 300
 CTGGCGGTGG CGGACCTCAT CCTGGTGGCC GACTCCCTCA TTGAGGTGTT CAACCTGCAC 360
 GAGCGGTACT ACGACATCGC CGTCCTGTGC ACCTTCATGT CGCTCTTCCT GCAGGTCAAC 420
 20 ATGTACAGCA GCGTCTTCTT CCTCACCTGG ATGAGCTTCG ACCGCTACAT CGCCCTGGCC 480
 AGGGCCATGC GCTGCAGCCT GTTCCGCACC AAGCACCACG CCCGGCTGAG CTGTGGCCTC 540
 ATCTGGATGG CATCCGTGTC AGCCACGCTG GTGCCCTTCA CCGCCGTGCA CCTGCAGCAC 600
 ACCGACGAGG CCTGCTTCTG TTTCGCGGAT GTCCGGGAGG TGCAGTGGCT CGAGGTCACG 660
 CTGGGCTTCA TCGTGCCCTT CGCCATCATC GGCCTGTGCT ACTCCCTCAT TGTCCGGGTG 720
 25 CTGGTCAGGG CGCACCAGCA CCGTGGGCTG CGCCCCGGC GGCAGAAGGC GAAGCGCATG 780
 ATCCTCGCGG TGGTGCTGGT CTTCTTCGTC TGCTGGCTGC CGGAGAACGT CTTTCATCAGC 840
 GTGCACCTCC TGCAGCGGAC GCAGCCTGGG GCCGCTCCCT GCAAGCAGTC TTTCCGCCAT 900
 GCCCACCCCC TCACGGGCCA CATTGTCAAC CTCACCGCCT TCTCCAACAG CTGCCTAAAC 960
 CCCCTCATCT ACAGCTTTCT CGGGGAGACC TTCAGGGACA AGCTGAGGCT GTACATTGAG 1020
 30 CAGAAAACAA ATTTGCCGGC CCTGAACCGC TTCTGTCACG CTGCCCTGAA GGCCGTCATT 1080
 CCAGACAGCA CCGAGCAGTC GGATGTGAGG TTCAGCAGTG CCGTGTAG 1128

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(203) INFORMATION FOR SEQ ID NO:202:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 375 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Met Asp Val Thr Ser Gln Ala Arg Gly Val Gly Leu Glu Met Tyr Pro
 1 5 10 15

Gly Thr Ala Gln Pro Ala Ala Pro Asn Thr Thr Ser Pro Glu Leu Asn
 20 25 30

Leu Ser His Pro Leu Leu Gly Thr Ala Leu Ala Asn Gly Thr Gly Glu
 35 40 45

Leu Ser Glu His Gln Gln Tyr Val Ile Gly Leu Phe Leu Ser Cys Leu
 50 55 60

Tyr Thr Ile Phe Leu Phe Pro Ile Gly Phe Val Gly Asn Ile Leu Ile
 65 70 75 80

Leu Val Val Asn Ile Ser Phe Arg Glu Lys Met Thr Ile Pro Asp Leu
 85 90 95

Tyr Phe Ile Asn Leu Ala Val Ala Asp Leu Ile Leu Val Ala Asp Ser
 100 105 110

Leu Ile Glu Val Phe Asn Leu His Glu Arg Tyr Tyr Asp Ile Ala Val
 115 120 125

Leu Cys Thr Phe Met Ser Leu Phe Leu Gln Val Asn Met Tyr Ser Ser
 130 135 140

Val Phe Phe Leu Thr Trp Met Ser Phe Asp Arg Tyr Ile Ala Leu Ala
 145 150 155 160

Arg Ala Met Arg Cys Ser Leu Phe Arg Thr Lys His His Ala Arg Leu
 165 170 175

Ser Cys Gly Leu Ile Trp Met Ala Ser Val Ser Ala Thr Leu Val Pro
 180 185 190

Phe Thr Ala Val His Leu Gln His Thr Asp Glu Ala Cys Phe Cys Phe
 195 200 205

Ala Asp Val Arg Glu Val Gln Trp Leu Glu Val Thr Leu Gly Phe Ile
 210 215 220

Val Pro Phe Ala Ile Ile Gly Leu Cys Tyr Ser Leu Ile Val Arg Val

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225 230 235 240
 Leu Val Arg Ala His Arg His Arg Gly Leu Arg Pro Arg Arg Gln Lys
 245 250 255
 5 Ala Lys Arg Met Ile Leu Ala Val Val Leu Val Phe Phe Val Cys Trp
 260 265 270
 Leu Pro Glu Asn Val Phe Ile Ser Val His Leu Leu Gln Arg Thr Gln
 275 280 285
 Pro Gly Ala Ala Pro Cys Lys Gln Ser Phe Arg His Ala His Pro Leu
 290 295 300
 10 Thr Gly His Ile Val Asn Leu Thr Ala Phe Ser Asn Ser Cys Leu Asn
 305 310 315 320
 Pro Leu Ile Tyr Ser Phe Leu Gly Glu Thr Phe Arg Asp Lys Leu Arg
 325 330 335
 15 Leu Tyr Ile Glu Gln Lys Thr Asn Leu Pro Ala Leu Asn Arg Phe Cys
 340 345 350
 His Ala Ala Leu Lys Ala Val Ile Pro Asp Ser Thr Glu Gln Ser Asp
 355 360 365
 Val Arg Phe Ser Ser Ala Val
 370 375
 20 (204) INFORMATION FOR SEQ ID NO:203:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1137 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 25 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:
 30 ATGGACCTGG GGAAACCAAT GAAAAGCGTG CTGGTGGTGG CTCTCCTTGT CATTTTCCAG 60
 GTATGCCTGT GTCAAGATGA GGTACGGAC GATTACATCG GAGACAACAC CACAGTGGAC 120
 TACACTTTGT TCGAGTCTTT GTGCTCCAAG AAGGACGTGC GGAAC TTAA AGCCTGGTTC 180
 CTCCCTATCA TGTACTCCAT CATTGTGTTT GTGGGCTTAC TGGGCAATGG GCTGGTCGTG 240
 TTGACCTATA TCTATTTCAA GAGGCTCAAG ACCATGACCG ATACCTACCT GCTCAACCTG 300
 GCGGTGGCAG ACATCCTCTT CCTCTGACC CTTCCCTTCT GGGCCTACAG CGCGGCCAAG 360
 TCCTGGGTCT TCGGTGTCCA CTTTGTGCAAG CTCATCTTTG CCATCTACAA GATGAGCTTC 420

TTCAGTGGCA TGCTCCTACT TCTTTCATC AGCATTGACC GCTACGTGGC CATCGTCCAG 480
 GCTGTCTCAG CTCACCGCCA CCGTGCCCGC GTCCTTCTCA TCAGCAAGCT GTCCTGTGTG 540
 GGCATCTGGA TACTAGCCAC AGTGCTCTCC ATCCCAGAGC TCCTGTACAG TGACCTCCAG 600
 AGGAGCAGCA GTGAGCAAGC GATGCGATGC TCTCTCATCA CAGAGCATGT GGAGGCCTTT 660
 5 ATCACCATCC AGGTGGCCCA GATGGTGATC GGCTTTCTGG TCCCCCTGCT GGCCATGAGC 720
 TTCTGTTACC TTGTCATCAT CCGCACCTG CTCCAGGCAC GCAACTTTGA GCGCAACAAG 780
 GCCAAAAAGG TGATCATCGC TGTGGTCGTG GTCTTCATAG TCTTCCAGCT GCCCTACAAT 840
 GGGGTGGTCC TGGCCAGAC GGTGGCCAAC TTCAACATCA CCAGTAGCAC CTGTGAGCTC 900
 AGTAAGCAAC TCAACATCGC CTACGACGTC ACCTACAGCC TGGCCTGCGT CCGCTGCTGC 960
 10 GTCAACCCTT TCTTGTACGC CTTTCATCGC GTCAAGTTCC GCAACGATCT CTTCAAGCTC 1020
 TTCAAGGACC TGGGCTGCCT CAGCCAGGAG CAGCTCCGGC AGTGGTCTTC CTGTCCGCAC 1080
 ATCCGGCGCT CCTCCATGAG TGTGGAGGCC GAGACCACCA CCACCTTCTC CCCATAG 1137

(205) INFORMATION FOR SEQ ID NO:204:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 378 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

- 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Met Asp Leu Gly Lys Pro Met Lys Ser Val Leu Val Val Ala Leu Leu
 1 5 10 15
 Val Ile Phe Gln Val Cys Leu Cys Gln Asp Glu Val Thr Asp Asp Tyr
 20 25 30
 25 Ile Gly Asp Asn Thr Thr Val Asp Tyr Thr Leu Phe Glu Ser Leu Cys
 35 40 45
 Ser Lys Lys Asp Val Arg Asn Phe Lys Ala Trp Phe Leu Pro Ile Met
 50 55 60
 30 Tyr Ser Ile Ile Cys Phe Val Gly Leu Leu Gly Asn Gly Leu Val Val
 65 70 75 80
 Leu Thr Tyr Ile Tyr Phe Lys Arg Leu Lys Thr Met Thr Asp Thr Tyr
 85 90 95
 Leu Leu Asn Leu Ala Val Ala Asp Ile Leu Phe Leu Leu Thr Leu Pro

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	100	105	110
	Phe Trp Ala Tyr Ser Ala Ala Lys Ser Trp Val Phe Gly Val His Phe		
	115	120	125
5	Cys Lys Leu Ile Phe Ala Ile Tyr Lys Met Ser Phe Phe Ser Gly Met		
	130	135	140
	Leu Leu Leu Leu Cys Ile Ser Ile Asp Arg Tyr Val Ala Ile Val Gln		
	145	150	155
	Ala Val Ser Ala His Arg His Arg Ala Arg Val Leu Leu Ile Ser Lys		
	165	170	175
10	Leu Ser Cys Val Gly Ile Trp Ile Leu Ala Thr Val Leu Ser Ile Pro		
	180	185	190
	Glu Leu Leu Tyr Ser Asp Leu Gln Arg Ser Ser Ser Glu Gln Ala Met		
	195	200	205
15	Arg Cys Ser Leu Ile Thr Glu His Val Glu Ala Phe Ile Thr Ile Gln		
	210	215	220
	Val Ala Gln Met Val Ile Gly Phe Leu Val Pro Leu Leu Ala Met Ser		
	225	230	235
	Phe Cys Tyr Leu Val Ile Ile Arg Thr Leu Leu Gln Ala Arg Asn Phe		
	245	250	255
20	Glu Arg Asn Lys Ala Lys Lys Val Ile Ile Ala Val Val Val Val Phe		
	260	265	270
	Ile Val Phe Gln Leu Pro Tyr Asn Gly Val Val Leu Ala Gln Thr Val		
	275	280	285
25	Ala Asn Phe Asn Ile Thr Ser Ser Thr Cys Glu Leu Ser Lys Gln Leu		
	290	295	300
	Asn Ile Ala Tyr Asp Val Thr Tyr Ser Leu Ala Cys Val Arg Cys Cys		
	305	310	315
	Val Asn Pro Phe Leu Tyr Ala Phe Ile Gly Val Lys Phe Arg Asn Asp		
	325	330	335
30	Leu Phe Lys Leu Phe Lys Asp Leu Gly Cys Leu Ser Gln Glu Gln Leu		
	340	345	350
	Arg Gln Trp Ser Ser Cys Arg His Ile Arg Arg Ser Ser Met Ser Val		
	355	360	365
35	Glu Ala Glu Thr Thr Thr Thr Phe Ser Pro		
	370	375	

(206) INFORMATION FOR SEQ ID NO:205:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1086 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

ATGGATATAC AAATGGCAAA CAATTTTACT CCGCCCTCTG CAACTCCTCA GGGAAATGAC 60
 TGTGACCTCT ATGCACATCA CAGCACGGCC AGGATAGTAA TGCCTCTGCA TTACAGCCTC 120
 10 GTCTTCATCA TTGGGCTCGT GGGAACTTA CTAGCCTTGG TCGTCATTGT TCAAAACAGG 180
 AAAAAAATCA ACTCTACCAC CCTCTATTCA ACAAATTGG TGATTTCTGA TATACTTTTT 240
 ACCACGGCTT TGCCTACACG AATAGCCTAC TATGCAATGG GCTTTGACTG GAGAATCGGA 300
 GATGCCTTGT GTAGGATAAC TGCGCTAGTG TTTTACATCA ACACATATGC AGGTGTGAAC 360
 TTTATGACCT GCCTGAGTAT TGACCGCTTC ATTGCTGTGG TGCACCCTCT ACGCTACAAC 420
 15 AAGATAAAAA GGATTGAACA TGCAAAAGGC GTGTGCATAT TTGTCTGGAT TCTAGTATTT 480
 GCTCAGACAC TCCCACTCCT CATCAACCCT ATGTCAAAGC AGGAGGCTGA AAGGATTACA 540
 TGCATGGAGT ATCCAAACTT TGAAGAACT AAATCTCTTC CCTGGATTCT GCTTGGGGCA 600
 TGTTCATAG GATATGTACT TCCACTTATA ATCATTCTCA TCTGCTATTC TCAGATCTGC 660
 TGCAAACTCT TCAGAACTGC CAAACAAAAC CCACTCACTG AGAAATCTGG TGTAACAAA 720
 20 AAGGCTAAAA ACACAATTAT TCTTATTATT GTTGTGTTTG TTCTCTGTTT CACACCTTAC 780
 CATGTTGCAA TTATTCAACA TATGATTAAG AAGCTTCGTT TCTCTAATT CCTGGAATGT 840
 AGCCAAAGAC ATTGTTCCA GATTTCTCTG CACTTTACAG TATGCCTGAT GAACTTCAAT 900
 TGCTGCATGG ACCCTTTTAT CTACTTCTTT GCATGTAAAG GGTATAAGAG AAAGGTTATG 960
 AGGATGCTGA AACGGCAAGT CAGTGTATCG ATTTCTAGTG CTGTGAAGTC AGCCCCTGAA 1020
 25 GAAAATTCAC GTGAAATGAC AGAAACGCAG ATGATGATAC ATTCCAAGTC TTCAAATGGA 1080
 AAGTGA 1086

(207) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

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(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

	Met	Asp	Ile	Gln	Met	Ala	Asn	Asn	Phe	Thr	Pro	Pro	Ser	Ala	Thr	Pro	
	1				5					10					15		
5	Gln	Gly	Asn	Asp	Cys	Asp	Leu	Tyr	Ala	His	His	Ser	Thr	Ala	Arg	Ile	
			20						25					30			
	Val	Met	Pro	Leu	His	Tyr	Ser	Leu	Val	Phe	Ile	Ile	Gly	Leu	Val	Gly	
		35						40					45				
10	Asn	Leu	Leu	Ala	Leu	Val	Val	Ile	Val	Gln	Asn	Arg	Lys	Lys	Ile	Asn	
		50					55					60					
	Ser	Thr	Thr	Leu	Tyr	Ser	Thr	Asn	Leu	Val	Ile	Ser	Asp	Ile	Leu	Phe	
	65					70				75					80		
	Thr	Thr	Ala	Leu	Pro	Thr	Arg	Ile	Ala	Tyr	Tyr	Ala	Met	Gly	Phe	Asp	
				85					90					95			
15	Trp	Arg	Ile	Gly	Asp	Ala	Leu	Cys	Arg	Ile	Thr	Ala	Leu	Val	Phe	Tyr	
			100					105					110				
	Ile	Asn	Thr	Tyr	Ala	Gly	Val	Asn	Phe	Met	Thr	Cys	Leu	Ser	Ile	Asp	
			115					120					125				
20	Arg	Phe	Ile	Ala	Val	Val	His	Pro	Leu	Arg	Tyr	Asn	Lys	Ile	Lys	Arg	
		130					135					140					
	Ile	Glu	His	Ala	Lys	Gly	Val	Cys	Ile	Phe	Val	Trp	Ile	Leu	Val	Phe	
	145					150				155					160		
	Ala	Gln	Thr	Leu	Pro	Leu	Leu	Ile	Asn	Pro	Met	Ser	Lys	Gln	Glu	Ala	
				165					170					175			
25	Glu	Arg	Ile	Thr	Cys	Met	Glu	Tyr	Pro	Asn	Phe	Glu	Glu	Thr	Lys	Ser	
			180						185					190			
	Leu	Pro	Trp	Ile	Leu	Leu	Gly	Ala	Cys	Phe	Ile	Gly	Tyr	Val	Leu	Pro	
			195				200						205				
30	Leu	Ile	Ile	Ile	Leu	Ile	Cys	Tyr	Ser	Gln	Ile	Cys	Cys	Lys	Leu	Phe	
		210					215					220					
	Arg	Thr	Ala	Lys	Gln	Asn	Pro	Leu	Thr	Glu	Lys	Ser	Gly	Val	Asn	Lys	
	225					230				235					240		
	Lys	Ala	Lys	Asn	Thr	Ile	Ile	Leu	Ile	Ile	Val	Val	Phe	Val	Leu	Cys	
				245					250					255			
35	Phe	Thr	Pro	Tyr	His	Val	Ala	Ile	Ile	Gln	His	Met	Ile	Lys	Lys	Leu	
				260					265					270			

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Arg Phe Ser Asn Phe Leu Glu Cys Ser Gln Arg His Ser Phe Gln Ile
 275 280 285

Ser Leu His Phe Thr Val Cys Leu Met Asn Phe Asn Cys Cys Met Asp
 290 295 300

5 Pro Phe Ile Tyr Phe Phe Ala Cys Lys Gly Tyr Lys Arg Lys Val Met
 305 310 315 320

Arg Met Leu Lys Arg Gln Val Ser Val Ser Ile Ser Ser Ala Val Lys
 325 330 335

10 Ser Ala Pro Glu Glu Asn Ser Arg Glu Met Thr Glu Thr Gln Met Met
 340 345 350

Ile His Ser Lys Ser Ser Asn Gly Lys
 355 360

(208) INFORMATION FOR SEQ ID NO:207:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1446 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

ATGCGGTGGC TGTGGCCCCT GGCTGTCTCT CTTGCTGTGA TTTTGGCTGT GGGGCTAAGC 60

AGGGTCTCTG GGGGTGCCCC CTTGCACCTG GGCAGGCACA GAGCCGAGAC CCAGGAGCAG 120

CAGAGCCGAT CCAAGAGGGG CACCGAGGAT GAGGAGGCCA AGGGCGTGCA GCAGTATGTG 180

CCTGAGGAGT GGGCGGAGTA CCCCCGGCCC ATTCAACCTG CTGGCCTGCA GCCAACCAAG 240

25 CCCTTGGTGG CCACCAGCCC TAACCCCGAC AAGGATGGGG GCACCCCAAG CAGTGGGCAG 300

GAACTGAGGG GCAATCTGAC AGGGGCACCA GGGCAGAGGC TACAGATCCA GAACCCCTG 360

TATCCGGTGA CCGAGAGCTC CTACAGTGCC TATGCCATCA TGCTTCTGGC GCTGGTGGTG 420

TTTGCGGTGG GCATTGTGGG CAACCTGTCTG GTCATGTGCA TCGTGTGGCA CAGCTACTAC 480

CTGAAGAGCG CCTGGAATC CATCCTTGCC AGCCTGGCCC TCTGGGATTT TCTGGTCCTC 540

30 TTTTCTTGCC TCCCTATTGT CATCTTCAAC GAGATCACCA AGCAGAGGCT ACTGGGTGAC 600

GTTTCTTGTC GTGCCGTGCC CTTTATGGAG GTCTCTCTC TGGGAGTCAC GACTTTTCAGC 660

CTCTGTGCCC TGGGCATTGA CCGCTTCCAC GTGGCCACCA GCACCCTGCC CAAGGTGAGG 720

CCCATCGAGC GGTGCCAATC CATCCTGGCC AAGTTGGCTG TCATCTGGGT GGGCTCCATG 780

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ACGCTGGCTG TGCCTGAGCT CCTGCTGTGG CAGCTGGCAC AGGAGCCTGC CCCCACCATG 840
 GGCACCCTGG ACTCATGCAT CATGAAACCC TCAGCCAGCC TGCCCGAGTC CCTGTATTCA 900
 CTGGTGATGA CCTACCAGAA CGCCCGCATG TGGTGGTACT TTGGCTGCTA CTTCTGCCTG 960
 CCCATCCTCT TCACAGTCAC CTGCCAGCTG GTGACATGGC GGGTGCGAGG CCCTCCAGGG 1020
 5 AGGAAGTCAG AGTGCAGGGC CAGCAAGCAC GAGCAGTGTG AGAGCCAGCT CAAGAGCACC 1080
 GTGGTGGGCC TGACCGTGGT CTACGCCTTC TGCACCCTCC CAGAGAACGT CTGCAACATC 1140
 GTGGTGGCCT ACCTCTCCAC CGAGCTGACC CGCCAGACCC TGGACCTCCT GGGCCTCATC 1200
 AACCAGTTCT CCACCTTCTT CAAGGGCGCC ATCACCCAG TGCTGCTCCT TTGCATCTGC 1260
 AGGCCGCTGG GCCAGGCCTT CCTGGACTGC TGCTGCTGCT GCTGCTGTGA GGAGTGCGGC 1320
 10 GGGGCTTCGG AGGCCTCTGC TGCCAATGGG TCGGACAACA AGCTCAAGAC CGAGGTGTCC 1380
 TCTTCCATCT ACTTCCACAA GCCCAGGGAG TCACCCCCAC TCCTGCCCCT GGGCACACCT 1440
 TGCTGA 1446

(209) INFORMATION FOR SEQ ID NO:208:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 481 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

- 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

Met Arg Trp Leu Trp Pro Leu Ala Val Ser Leu Ala Val Ile Leu Ala
 1 5 10 15
 Val Gly Leu Ser Arg Val Ser Gly Gly Ala Pro Leu His Leu Gly Arg
 20 25 30
 25 His Arg Ala Glu Thr Gln Glu Gln Ser Arg Ser Lys Arg Gly Thr
 35 40 45
 Glu Asp Glu Glu Ala Lys Gly Val Gln Gln Tyr Val Pro Glu Glu Trp
 50 55 60
 30 Ala Glu Tyr Pro Arg Pro Ile His Pro Ala Gly Leu Gln Pro Thr Lys
 65 70 75 80
 Pro Leu Val Ala Thr Ser Pro Asn Pro Asp Lys Asp Gly Gly Thr Pro
 85 90 95
 Asp Ser Gly Gln Glu Leu Arg Gly Asn Leu Thr Gly Ala Pro Gly Gln

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	100	105	110
	Arg Leu Gln Ile Gln Asn Pro Leu Tyr Pro Val Thr Glu Ser Ser Tyr 115 120 125		
5	Ser Ala Tyr Ala Ile Met Leu Leu Ala Leu Val Val Phe Ala Val Gly 130 135 140		
	Ile Val Gly Asn Leu Ser Val Met Cys Ile Val Trp His Ser Tyr Tyr 145 150 155 160		
	Leu Lys Ser Ala Trp Asn Ser Ile Leu Ala Ser Leu Ala Leu Trp Asp 165 170 175		
10	Phe Leu Val Leu Phe Phe Cys Leu Pro Ile Val Ile Phe Asn Glu Ile 180 185 190		
	Thr Lys Gln Arg Leu Leu Gly Asp Val Ser Cys Arg Ala Val Pro Phe 195 200 205		
15	Met Glu Val Ser Ser Leu Gly Val Thr Thr Phe Ser Leu Cys Ala Leu 210 215 220		
	Gly Ile Asp Arg Phe His Val Ala Thr Ser Thr Leu Pro Lys Val Arg 225 230 235 240		
	Pro Ile Glu Arg Cys Gln Ser Ile Leu Ala Lys Leu Ala Val Ile Trp 245 250 255		
20	Val Gly Ser Met Thr Leu Ala Val Pro Glu Leu Leu Leu Trp Gln Leu 260 265 270		
	Ala Gln Glu Pro Ala Pro Thr Met Gly Thr Leu Asp Ser Cys Ile Met 275 280 285		
25	Lys Pro Ser Ala Ser Leu Pro Glu Ser Leu Tyr Ser Leu Val Met Thr 290 295 300		
	Tyr Gln Asn Ala Arg Met Trp Trp Tyr Phe Gly Cys Tyr Phe Cys Leu 305 310 315 320		
	Pro Ile Leu Phe Thr Val Thr Cys Gln Leu Val Thr Trp Arg Val Arg 325 330 335		
30	Gly Pro Pro Gly Arg Lys Ser Glu Cys Arg Ala Ser Lys His Glu Gln 340 345 350		
	Cys Glu Ser Gln Leu Lys Ser Thr Val Val Gly Leu Thr Val Val Tyr 355 360 365		
35	Ala Phe Cys Thr Leu Pro Glu Asn Val Cys Asn Ile Val Val Ala Tyr 370 375 380		
	Leu Ser Thr Glu Leu Thr Arg Gln Thr Leu Asp Leu Leu Gly Leu Ile 385 390 395 400		

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Asn Gln Phe Ser Thr Phe Phe Lys Gly Ala Ile Thr Pro Val Leu Leu
 405 410 415
 Leu Cys Ile Cys Arg Pro Leu Gly Gln Ala Phe Leu Asp Cys Cys Cys
 420 425 430
 5 Cys Cys Cys Cys Glu Glu Cys Gly Gly Ala Ser Glu Ala Ser Ala Ala
 435 440 445
 Asn Gly Ser Asp Asn Lys Leu Lys Thr Glu Val Ser Ser Ser Ile Tyr
 450 455 460
 10 Phe His Lys Pro Arg Glu Ser Pro Pro Leu Leu Pro Leu Gly Thr Pro
 465 470 475 480
 Cys

(210) INFORMATION FOR SEQ ID NO:209:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1101 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

ATGTGGAACG CGACGCCCAG CGAAGAGCCG GGGTTCAACC TCACACTGGC CGACCTGGAC 60
 TGGGATGCTT CCCCCGGCAA CGACTCGCTG GGCACGAGC TGCTGCAGCT CTTCCCCGCG 120
 CCGCTGCTGG CGGGCGTCAC AGCCACCTGC GTGGCACTCT TCGTGGTGGG TATCGCTGGC 180
 AACCTGCTCA CCATGCTGGT GGTGTCGCGC TTCCGCGAGC TGCGCACCAC CACCAACCTC 240
 25 TACCTGTCCA GCATGGCCTT CTCGATCTG CTCATCTTCC TCTGCATGCC CCTGGACCTC 300
 GTTCGCCTCT GGCAGTACCG GCCCTGGAAC TTCGGCGACC TCCTCTGCAA ACTCTTCCAA 360
 TTCGTCAGTG AGAGCTGCAC CTACGCCACG GTGCTCACCA TCACAGCGCT GAGCGTCGAG 420
 CGCTACTTCG CCATCTGCTT CCCACTCCGG GCCAAGGTGG TGGTCACCAA GGGGCGGGTG 480
 AAGCTGGTCA TCTTCGTCAT CTGGGCCGTC GCCTTCTGCA GCGCCGGGCC CATCTTCGTG 540
 30 CTAGTCGGGG TGGAGCACGA GAACGGCACC GACCCTTGGG ACACCAACGA GTGCCGCCCC 600
 ACCGAGTTTG CGGTGCGCTC TGGACTGCTC ACGGTCATGG TGTGGGTGTC CAGCATCTTC 660
 TTCTTCCTTC CTGTCTTCTG TCTCACGGTC CTCTACAGTC TCATCGGCAG GAAGCTGTGG 720
 CGGAGGAGGC GCGGCGATGC TGTGCTGGGT GCCTCGCTCA GGGACCAGAA CCACAAGCAA 780

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ACCAAGAAAA TGCTGGCTGT AGTGGTGTTC GCCTTCATCC TCTGCTGGCT CCCCTTCCAC 840
 GTAGGGCGAT ATTTATTTTC CAAATCCTTT GAGCCTGGCT CCTTGAGAT TGCTCAGATC 900
 AGCCAGTACT GCAACCTCGT GTCCTTTGTC CTCTTCTACC TCAGTGCTGC CATCAACCCC 960
 ATTCTGTACA ACATCATGTC CAAGAAGTAC CGGGTGGCAG TGTTCAGACT TCTGGGATTC 1020
 5 GAACCCTTCT CCCAGAGAAA GCTCTCCACT CTGAAAGATG AAAGTTCTCG GGCCTGGACA 1080
 GAATCTAGTA TTAATACATG A 1101

(211) INFORMATION FOR SEQ ID NO:210:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 366 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

15 Met Trp Asn Ala Thr Pro Ser Glu Glu Pro Gly Phe Asn Leu Thr Leu
 1 5 10 15
 Ala Asp Leu Asp Trp Asp Ala Ser Pro Gly Asn Asp Ser Leu Gly Asp
 20 25 30
 20 Glu Leu Leu Gln Leu Phe Pro Ala Pro Leu Leu Ala Gly Val Thr Ala
 35 40 45
 Thr Cys Val Ala Leu Phe Val Val Gly Ile Ala Gly Asn Leu Leu Thr
 50 55 60
 Met Leu Val Val Ser Arg Phe Arg Glu Leu Arg Thr Thr Thr Asn Leu
 65 70 75 80
 25 Tyr Leu Ser Ser Met Ala Phe Ser Asp Leu Leu Ile Phe Leu Cys Met
 85 90 95
 Pro Leu Asp Leu Val Arg Leu Trp Gln Tyr Arg Pro Trp Asn Phe Gly
 100 105 110
 30 Asp Leu Leu Cys Lys Leu Phe Gln Phe Val Ser Glu Ser Cys Thr Tyr
 115 120 125
 Ala Thr Val Leu Thr Ile Thr Ala Leu Ser Val Glu Arg Tyr Phe Ala
 130 135 140
 Ile Cys Phe Pro Leu Arg Ala Lys Val Val Val Thr Lys Gly Arg Val
 145 150 155 160
 35 Lys Leu Val Ile Phe Val Ile Trp Ala Val Ala Phe Cys Ser Ala Gly

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		165		170		175										
	Pro	Ile	Phe	Val	Leu	Val	Gly	Val	Glu	His	Glu	Asn	Gly	Thr	Asp	Pro
				180					185						190	
5	Trp	Asp	Thr	Asn	Glu	Cys	Arg	Pro	Thr	Glu	Phe	Ala	Val	Arg	Ser	Gly
			195				200						205			
	Leu	Leu	Thr	Val	Met	Val	Trp	Val	Ser	Ser	Ile	Phe	Phe	Phe	Leu	Pro
		210					215					220				
	Val	Phe	Cys	Leu	Thr	Val	Leu	Tyr	Ser	Leu	Ile	Gly	Arg	Lys	Leu	Trp
	225				230					235					240	
10	Arg	Arg	Arg	Arg	Gly	Asp	Ala	Val	Val	Gly	Ala	Ser	Leu	Arg	Asp	Gln
					245					250					255	
	Asn	His	Lys	Gln	Thr	Lys	Lys	Met	Leu	Ala	Val	Val	Val	Phe	Ala	Phe
			260					265						270		
15	Ile	Leu	Cys	Trp	Leu	Pro	Phe	His	Val	Gly	Arg	Tyr	Leu	Phe	Ser	Lys
		275					280						285			
	Ser	Phe	Glu	Pro	Gly	Ser	Leu	Glu	Ile	Ala	Gln	Ile	Ser	Gln	Tyr	Cys
		290					295					300				
	Asn	Leu	Val	Ser	Phe	Val	Leu	Phe	Tyr	Leu	Ser	Ala	Ala	Ile	Asn	Pro
	305					310				315					320	
20	Ile	Leu	Tyr	Asn	Ile	Met	Ser	Lys	Lys	Tyr	Arg	Val	Ala	Val	Phe	Arg
				325						330					335	
	Leu	Leu	Gly	Phe	Glu	Pro	Phe	Ser	Gln	Arg	Lys	Leu	Ser	Thr	Leu	Lys
			340					345						350		
25	Asp	Glu	Ser	Ser	Arg	Ala	Trp	Thr	Glu	Ser	Ser	Ile	Asn	Thr		
		355					360						365			

(212) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1842 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

	ATGCGAGCCC	CGGGCGCGCT	TCTCGCCCGC	ATGTCGCGGC	TACTGCTTCT	GCTACTGCTC	60
35	AAGGTGTCTG	CCTCTTCTGC	CCTCGGGGTC	GCCCTGCGT	CCAGAAACGA	AACTTGCTG	120
	GGGAGAGCT	GTGCACCTAC	AGTGATCCAG	CGCCGCGGCA	GGGACGCCTG	GGGACCGGGA	180

	AATTCTGCAA GAGACGTTCT GCGAGCCCGA GCACCCAGGG AGGAGCAGGG GGCAGCGTTT	240
	CTTGCGGGAC CCTCCTGGGA CTGCCGGCG GCCCCGGGCC GTGACCCGGC TGCAGGCAGA	300
	GGGGCGGAGG CGTCGGCAGC CGGACCCCCG GGACCTCCAA CCAGGCCACC TGGCCCCTGG	360
	AGGTGGAAG GTGCTCGGG TCAGGAGCCT TCTGAAACTT TGGGGAGAGG GAACCCACG	420
5	GCCCTCCAGC TCTTCCTTCA GATCTCAGAG GAGGAAGAGA AGGGTCCCAG AGGCGCTGGC	480
	ATTTCCGGGC GTAGCCAGGA GCAGAGTGTG AAGACAGTCC CCGGAGCCAG CGATCTTTTT	540
	TACTGGCCAA GGAGAGCCGG GAAACTCCAG GGTTCCCACC ACAAGCCCCT GTCCAAGACG	600
	GCCAATGGAC TGGCGGGGCA CGAAGGGTGG ACAATTGCAC TCCCGGGCCG GCGCTGGCC	660
	CAGAATGGAT CCTTGGGTGA AGGAATCCAT GAGCCTGGGG GTCCCCGCCG GGGAAACAGC	720
10	ACGAACCGGC GTGTGAGACT GAAGAACCCC TTCTACCCGC TGACCCAGGA GTCCTATGGA	780
	GCCTACGCGG TCATGTGTCT GTCCGTGGTG ATCTTCGGGA CCGGCATCAT TGGCAACCTG	840
	GCGGTGATGT GCATCGTGTG CCACAACCTAC TACATGCGGA GCATCTCCAA CTCCTCTTG	900
	GCCAACCTGG CTTTCTGGGA CTTTCTCATC ATCTTCTTCT GCCTTCGCT GGTCTCTTC	960
	CACGAGCTGA CCAAGAAGTG GCTGCTGGAG GACTTCTCCT GCAAGATCGT GCCCTATATA	1020
15	GAGGTGCGCT CTCTGGGAGT CACCACTTTC ACCTTATGTG CTCTGTGCAT AGACCGCTTC	1080
	CGTGCTGCCA CCAACGTACA GATGTACTAC GAAATGATCG AAAATTGTTC CTCAACAAC	1140
	GCCAAACTTG CTGTTATATG GGTGGGAGCT CTATTGTTAG CACTTCCAGA AGTTGTTCTC	1200
	CGCCAGCTGA GCAAGGAGGA TTTGGGGTTT AGTGGCCGAG CTCGGCAGA AAGGTGCATT	1260
	ATTAAGATCT CTCCTGATTT ACCAGACACC ATCTATGTTC TAGCCCTCAC CTACGACAGT	1320
20	GCGAGACTGT GGTGGTATTT TGGCTGTTAC TTTTGTTCG CCACGCTTTT CACCATCACC	1380
	TGCTCTCTAG TGAAGTGGAG GAAAATCCGC AAAGCAGAGA AAGCCTGTAC CCGAGGGAAT	1440
	AAACGGCAGA TTCAACTAGA GAGTCAGATG AAGTGTACAG TAGTGGCACT GACCATTTTA	1500
	TATGGATTTT GCATTATTCC TGAAAATATC TGCAACATTG TTAAGTGCCTA CATGGCTACA	1560
	GGGGTTTCAC AGCAGACAAT GGACCTCCTT AATATCATCA GCCAGTTCCT TTTGTTCTTT	1620
25	AAGTCCTGTG TCACCCAGT CCTCCTTTTC TGTCTCTGCA AACCCCTCAG TCGGGCCTTC	1680
	ATGGAGTGCT GCTGCTGTTG CTGTGAGGAA TGCATTGAGA AGTCTTCAAC GGTGACCAGT	1740
	GATGACAATG ACAACGAGTA CACCACGGAA CTCGAACTCT CGCCTTTCAG TACCATACGC	1800
	CGTGAAATGT CCACTTTTGC TTCTGTGCGA ACTCATTGCT GA	1842

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(213) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 613 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

10 Met Arg Ala Pro Gly Ala Leu Leu Ala Arg Met Ser Arg Leu Leu Leu
 1 5 10 15
 Leu Leu Leu Leu Lys Val Ser Ala Ser Ser Ala Leu Gly Val Ala Pro
 20 25 30
 Ala Ser Arg Asn Glu Thr Cys Leu Gly Glu Ser Cys Ala Pro Thr Val
 35 40 45
 15 Ile Gln Arg Arg Gly Arg Asp Ala Trp Gly Pro Gly Asn Ser Ala Arg
 50 55 60
 Asp Val Leu Arg Ala Arg Ala Pro Arg Glu Glu Gln Gly Ala Ala Phe
 65 70 75 80
 20 Leu Ala Gly Pro Ser Trp Asp Leu Pro Ala Ala Pro Gly Arg Asp Pro
 85 90 95
 Ala Ala Gly Arg Gly Ala Glu Ala Ser Ala Ala Gly Pro Pro Gly Pro
 100 105 110
 Pro Thr Arg Pro Pro Gly Pro Trp Arg Trp Lys Gly Ala Arg Gly Gln
 115 120 125
 25 Glu Pro Ser Glu Thr Leu Gly Arg Gly Asn Pro Thr Ala Leu Gln Leu
 130 135 140
 Phe Leu Gln Ile Ser Glu Glu Glu Glu Lys Gly Pro Arg Gly Ala Gly
 145 150 155 160
 30 Ile Ser Gly Arg Ser Gln Glu Gln Ser Val Lys Thr Val Pro Gly Ala
 165 170 175
 Ser Asp Leu Phe Tyr Trp Pro Arg Arg Ala Gly Lys Leu Gln Gly Ser
 180 185 190
 His His Lys Pro Leu Ser Lys Thr Ala Asn Gly Leu Ala Gly His Glu
 195 200 205
 35 Gly Trp Thr Ile Ala Leu Pro Gly Arg Ala Leu Ala Gln Asn Gly Ser
 210 215 220
 Leu Gly Glu Gly Ile His Glu Pro Gly Gly Pro Arg Arg Gly Asn Ser

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	225		230		235		240									
	Thr	Asn	Arg	Arg	Val	Arg	Leu	Lys	Asn	Pro	Phe	Tyr	Pro	Leu	Thr	Gln
				245					250						255	
5	Glu	Ser	Tyr	Gly	Ala	Tyr	Ala	Val	Met	Cys	Leu	Ser	Val	Val	Ile	Phe
				260					265					270		
	Gly	Thr	Gly	Ile	Ile	Gly	Asn	Leu	Ala	Val	Met	Cys	Ile	Val	Cys	His
			275					280					285			
	Asn	Tyr	Tyr	Met	Arg	Ser	Ile	Ser	Asn	Ser	Leu	Leu	Ala	Asn	Leu	Ala
		290					295					300				
10	Phe	Trp	Asp	Phe	Leu	Ile	Ile	Phe	Phe	Cys	Leu	Pro	Leu	Val	Ile	Phe
	305					310					315				320	
	His	Glu	Leu	Thr	Lys	Lys	Trp	Leu	Leu	Glu	Asp	Phe	Ser	Cys	Lys	Ile
					325					330					335	
15	Val	Pro	Tyr	Ile	Glu	Val	Ala	Ser	Leu	Gly	Val	Thr	Thr	Phe	Thr	Leu
				340					345					350		
	Cys	Ala	Leu	Cys	Ile	Asp	Arg	Phe	Arg	Ala	Ala	Thr	Asn	Val	Gln	Met
		355					360						365			
	Tyr	Tyr	Glu	Met	Ile	Glu	Asn	Cys	Ser	Ser	Thr	Thr	Ala	Lys	Leu	Ala
		370				375						380				
20	Val	Ile	Trp	Val	Gly	Ala	Leu	Leu	Leu	Ala	Leu	Pro	Glu	Val	Val	Leu
	385				390						395				400	
	Arg	Gln	Leu	Ser	Lys	Glu	Asp	Leu	Gly	Phe	Ser	Gly	Arg	Ala	Pro	Ala
				405					410					415		
25	Glu	Arg	Cys	Ile	Ile	Lys	Ile	Ser	Pro	Asp	Leu	Pro	Asp	Thr	Ile	Tyr
			420					425					430			
	Val	Leu	Ala	Leu	Thr	Tyr	Asp	Ser	Ala	Arg	Leu	Trp	Trp	Tyr	Phe	Gly
		435					440					445				
	Cys	Tyr	Phe	Cys	Leu	Pro	Thr	Leu	Phe	Thr	Ile	Thr	Cys	Ser	Leu	Val
		450				455						460				
30	Thr	Ala	Arg	Lys	Ile	Arg	Lys	Ala	Glu	Lys	Ala	Cys	Thr	Arg	Gly	Asn
	465				470					475					480	
	Lys	Arg	Gln	Ile	Gln	Leu	Glu	Ser	Gln	Met	Lys	Cys	Thr	Val	Val	Ala
				485					490					495		
35	Leu	Thr	Ile	Leu	Tyr	Gly	Phe	Cys	Ile	Ile	Pro	Glu	Asn	Ile	Cys	Asn
		500						505					510			
	Ile	Val	Thr	Ala	Tyr	Met	Ala	Thr	Gly	Val	Ser	Gln	Gln	Thr	Met	Asp
		515					520					525				

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Leu Leu Asn Ile Ile Ser Gln Phe Leu Leu Phe Phe Lys Ser Cys Val
 530 535 540
 Thr Pro Val Leu Leu Phe Cys Leu Cys Lys Pro Phe Ser Arg Ala Phe
 545 550 555 560
 5 Met Glu Cys Cys Cys Cys Cys Cys Glu Glu Cys Ile Gln Lys Ser Ser
 565 570 575
 Thr Val Thr Ser Asp Asp Asn Asp Asn Glu Tyr Thr Thr Glu Leu Glu
 580 585 590
 10 Leu Ser Pro Phe Ser Thr Ile Arg Arg Glu Met Ser Thr Phe Ala Ser
 595 600 605
 Val Gly Thr His Cys
 610

(214) INFORMATION FOR SEQ ID NO:213:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1248 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

ATGGTTTTTG CTCACAGAAT GGATAACAGC AAGCCACATT TGATTATTCC TACACTTCTG 60
 GTGCCCCTCC AAAACCGCAG CTGCACTGAA ACAGCCACAC CTCTGCCAAG CCAATACCTG 120
 ATGGAATTAA GTGAGGAGCA CAGTTGGATG AGCAACCAAA CAGACCTTCA CTATGTGCTG 180
 AAACCCGGGG AAGTGGCCAC AGCCAGCATC TTCTTTGGGA TTCTGTGGTT GTTTTCTATC 240
 25 TTCGGCAATT CCTGGTTTG TTTGGTCATC CATAGGAGTA GGAGGACTCA GTCTACCACC 300
 AACTACTTTG TGGTCTCCAT GGCATGTGCT GACCTTCTCA TCAGCGTTGC CAGCACGCCT 360
 TTCGTCTGTC TCCAGTTCAC CACTGGAAGG TGGACGCTGG GTAGTGCAAC GTGCAAGGTT 420
 GTGCGATATT TTCAATATCT CACTCCAGGT GTCCAGATCT ACGTTCTCCT CTCCATCTGC 480
 ATAGACCGGT TCTACACCAT CGTCTATCCT CTGAGCTTCA AGGTGTCCAG AGAAAAAGCC 540
 30 AAGAAAATGA TTGCGGCATC GTGGATCTTT GATGCAGGCT TTGTGACCCC TGTGCTCTTT 600
 TTCTATGGCT CCAACTGGGA CAGTCATTGT AACTATTTC TCCCCTCCTC TTGGGAAGGC 660
 ACTGCCTACA CTGTCATCCA CTTCTTGGTG GGCTTGTGA TTCCATCTGT CCTCATAATT 720
 TTATTTTACC AAAAGGTCAT AAAATATATT TGGAGAATAG GCACAGATGG CCGAACGGTG 780

AGGAGGACAA TGAACATTGT CCCTCGGACA AAAGTGAAAA CTAAAAAGAT GTTCCTCATT 840
 TTAAATCTGT TGTTTTGTCT CTCCTGGCTG CCTTTTCATG TAGCTCAGCT ATGGCACCCC 900
 CATGAACAAG ACTATAAGAA AAGTTCCTTT GTTTTCACAG CTATCACATG GATATCCTTT 960
 AGTTCTTCAG CCTCTAAACC TACTCTGTAT TCAATTTATA ATGCCAATTT TCGGAGAGGG 1020
 5 ATGAAAGAGA CTTTTTGCAT GTCCTCTATG AAATGTTACC GAAGCAATGC CTATACTATC 1080
 ACAACAAGTT CAAGGATGGC CAAAAAAAC TACGTTGGCA TTTCAGAAAT CCCTTCCATG 1140
 GCCAAACTA TTACCAAAGA CTCGATCTAT GACTCATTTG ACAGAGAAGC CAAGGAAAAA 1200
 AAGCTTGCTT GGCCCATTA CTCAAATCCA CCAATACTT TTGTCTAA 1248

(215) INFORMATION FOR SEQ ID NO:214:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 415 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant
- 15 (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:
- | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Val | Phe | Ala | His | Arg | Met | Asp | Asn | Ser | Lys | Pro | His | Leu | Ile | Ile | 1 | 5 | 10 | 15 |
| Pro | Thr | Leu | Leu | Val | Pro | Leu | Gln | Asn | Arg | Ser | Cys | Thr | Glu | Thr | Ala | 20 | 25 | 30 | |
| Thr | Pro | Leu | Pro | Ser | Gln | Tyr | Leu | Met | Glu | Leu | Ser | Glu | Glu | His | Ser | 35 | 40 | 45 | |
| Trp | Met | Ser | Asn | Gln | Thr | Asp | Leu | His | Tyr | Val | Leu | Lys | Pro | Gly | Glu | 50 | 55 | 60 | |
| Val | Ala | Thr | Ala | Ser | Ile | Phe | Phe | Gly | Ile | Leu | Trp | Leu | Phe | Ser | Ile | 65 | 70 | 75 | 80 |
| Phe | Gly | Asn | Ser | Leu | Val | Cys | Leu | Val | Ile | His | Arg | Ser | Arg | Arg | Thr | 85 | 90 | 95 | |
| Gln | Ser | Thr | Thr | Asn | Tyr | Phe | Val | Val | Ser | Met | Ala | Cys | Ala | Asp | Leu | 100 | 105 | 110 | |
| Leu | Ile | Ser | Val | Ala | Ser | Thr | Pro | Phe | Val | Leu | Leu | Gln | Phe | Thr | Thr | 115 | 120 | 125 | |
| Gly | Arg | Trp | Thr | Leu | Gly | Ser | Ala | Thr | Cys | Lys | Val | Val | Arg | Tyr | Phe | 130 | 135 | 140 | |

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Gln Tyr Leu Thr Pro Gly Val Gln Ile Tyr Val Leu Leu Ser Ile Cys
 145 150 155 160
 Ile Asp Arg Phe Tyr Thr Ile Val Tyr Pro Leu Ser Phe Lys Val Ser
 165 170 175
 5 Arg Glu Lys Ala Lys Lys Met Ile Ala Ala Ser Trp Ile Phe Asp Ala
 180 185 190
 Gly Phe Val Thr Pro Val Leu Phe Phe Tyr Gly Ser Asn Trp Asp Ser
 195 200 205
 10 His Cys Asn Tyr Phe Leu Pro Ser Ser Trp Glu Gly Thr Ala Tyr Thr
 210 215 220
 Val Ile His Phe Leu Val Gly Phe Val Ile Pro Ser Val Leu Ile Ile
 225 230 235 240
 Leu Phe Tyr Gln Lys Val Ile Lys Tyr Ile Trp Arg Ile Gly Thr Asp
 245 250 255
 15 Gly Arg Thr Val Arg Arg Thr Met Asn Ile Val Pro Arg Thr Lys Val
 260 265 270
 Lys Thr Lys Lys Met Phe Leu Ile Leu Asn Leu Leu Phe Leu Leu Ser
 275 280 285
 20 Trp Leu Pro Phe His Val Ala Gln Leu Trp His Pro His Glu Gln Asp
 290 295 300
 Tyr Lys Lys Ser Ser Leu Val Phe Thr Ala Ile Thr Trp Ile Ser Phe
 305 310 315 320
 Ser Ser Ser Ala Ser Lys Pro Thr Leu Tyr Ser Ile Tyr Asn Ala Asn
 325 330 335
 25 Phe Arg Arg Gly Met Lys Glu Thr Phe Cys Met Ser Ser Met Lys Cys
 340 345 350
 Tyr Arg Ser Asn Ala Tyr Thr Ile Thr Thr Ser Ser Arg Met Ala Lys
 355 360 365
 30 Lys Asn Tyr Val Gly Ile Ser Glu Ile Pro Ser Met Ala Lys Thr Ile
 370 375 380
 Thr Lys Asp Ser Ile Tyr Asp Ser Phe Asp Arg Glu Ala Lys Glu Lys
 385 390 395 400
 Lys Leu Ala Trp Pro Ile Asn Ser Asn Pro Pro Asn Thr Phe Val
 405 410 415

35 (216) INFORMATION FOR SEQ ID NO:215:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1842 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

ATGGGGCCCA	CCCTAGCGGT	TCCCACCCCC	TATGGCTGTA	TTGGCTGTAA	GCTACCCAG	60
CCAGAATACC	CACCGGCTCT	AATCATCTTT	ATGTTCTGCG	CGATGGTTAT	CACCATCGTT	120
GTAGACCTAA	TCGGCAACTC	CATGGTCATT	TTGGCTGTGA	CGAAGAACAA	GAAGCTCCGG	180
AATTCTGGCA	ACATCTTCGT	GGTCAGTCTC	TCTGTGGCCG	ATATGCTGGT	GGCCATCTAC	240
10 CCATACCCTT	TGATGCTGCA	TGCCATGTCC	ATTGGGGGCT	GGGATCTGAG	CCAGTTACAG	300
TGCCAGATGG	TCGGGTTTCAT	CACAGGGCTG	AGTGTGGTCG	GCTCCATCTT	CAACATCGTG	360
GCAATCGCTA	TCAACCGTTA	CTGCTACATC	TGCCACAGCC	TCCAGTACGA	ACGGATCTTC	420
AGTGTGCGCA	ATACCTGCAT	CTACCTGGTC	ATCACCTGGA	TCATGACCGT	CCTGGCTGTC	480
CTGCCCAACA	TGTACATTGG	CACCATCGAG	TACGATCCTC	GCACCTACAC	CTGCATCTTC	540
15 AACTATCTGA	ACAACCCTGT	CTTCACTGTT	ACCATCGTCT	GCATCCACTT	CGTCCTCCCT	600
CTCCTCATCG	TGGGTTTCTG	CTACGTGAGG	ATCTGGACCA	AAGTGCTGGC	GGCCCCGTGAC	660
CCTGCAGGGC	AGAATCCTGA	CAACCAACTT	GCTGAGGTTC	GCAATAAACT	AACCATGTTT	720
GTGATCTTCC	TCCTCTTTGC	AGTGTGCTGG	TGCCCTATCA	ACGTGCTCAC	TGTCTTGGTG	780
GCTGTCAGTC	CGAAGGAGAT	GGCAGGCAAG	ATCCCCAACT	GGCTTTATCT	TGCAGCCTAC	840
20 TTCATAGCCT	ACTTCAACAG	CTGCCTCAAC	GCTGTGATCT	ACGGGCTCCT	CAATGAGAAT	900
TTCCGAAGAG	AATACTGGAC	CATCTTCCAT	GCTATGCGGC	ACCCTATCAT	ATTCTTCTCT	960
GGCCTCATCA	GTGATATTCG	TGAGATGCAG	GAGGCCCGTA	CCCTGGCCCG	CGCCCCGTGCC	1020
CATGCTCGCG	ACCAAGCTCG	TGAACAAGAC	CGTGCCCATG	CCTGTCCTGC	TGTGGAGGAA	1080
ACCCCGATGA	ATGTCCGGAA	TGTTCCATTA	CCTGGTGATG	CTGCAGCTGG	CCACCCCGAC	1140
25 CGTGCCTCTG	GCCACCCTAA	GCCCCATTCC	AGATCCTCCT	CTGCCTATCG	CAAATCTGCC	1200
TCTACCCACC	ACAAGTCTGT	CTTTAGCCAC	TCCAAGGCTG	CCTCTGGTCA	CCTCAAGCCT	1260
GTCTCTGGCC	ACTCCAAGCC	TGCCTCTGGT	CACCCCAAGT	CTGCCACTGT	CTACCCTAAG	1320
CCTGCCTCTG	TCCATTTCAA	GGCTGACTCT	GTCCATTTCA	AGGGTGACTC	TGTCCATTTC	1380
AAGCCTGACT	CTGTTCAATT	CAAGCCTGCT	TCCAGCAACC	CCAAGCCCAT	CACTGGCCAC	1440

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CATGTCTCTG CTGGCAGCCA CTCCAAGTCT GCCTTCAATG CTGCCACCAG CCACCCTAAA 1500
 CCCATCAAGC CAGCTACCAG CCATGCTGAG CCCACCACTG CTGACTATCC CAAGCCTGCC 1560
 ACTACCAGCC ACCCTAAGCC CGCTGCTGCT GACAACCCCTG AGCTCTCTGC CTCCCATTGC 1620
 CCCGAGATCC CTGCCATTGC CCACCCTGTG TCTGACGACA GTGACCTCCC TGAGTCGGCC 1680
 5 TCTAGCCCTG CCGCTGGGCC CACCAAGCCT GCTGCCAGCC AGCTGGAGTC TGACACCATC 1740
 GCTGACCTTC CTGACCCTAC TGTAGTCACT ACCAGTACCA ATGATTACCA TGATGTCGTG 1800
 GTTGTTGATG TTGAAGATGA TCCTGATGAA ATGGCTGTGT GA 1842

(217) INFORMATION FOR SEQ ID NO:216:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 613 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

- 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

Met Gly Pro Thr Leu Ala Val Pro Thr Pro Tyr Gly Cys Ile Gly Cys
 1 5 10 15
 Lys Leu Pro Gln Pro Glu Tyr Pro Pro Ala Leu Ile Ile Phe Met Phe
 20 25 30
 Cys Ala Met Val Ile Thr Ile Val Val Asp Leu Ile Gly Asn Ser Met
 35 40 45
 Val Ile Leu Ala Val Thr Lys Asn Lys Lys Leu Arg Asn Ser Gly Asn
 50 55 60
 Ile Phe Val Val Ser Leu Ser Val Ala Asp Met Leu Val Ala Ile Tyr
 25 65 70 75 80
 Pro Tyr Pro Leu Met Leu His Ala Met Ser Ile Gly Gly Trp Asp Leu
 85 90 95
 Ser Gln Leu Gln Cys Gln Met Val Gly Phe Ile Thr Gly Leu Ser Val
 100 105 110
 Val Gly Ser Ile Phe Asn Ile Val Ala Ile Ala Ile Asn Arg Tyr Cys
 30 115 120 125
 Tyr Ile Cys His Ser Leu Gln Tyr Glu Arg Ile Phe Ser Val Arg Asn
 130 135 140
 Thr Cys Ile Tyr Leu Val Ile Thr Trp Ile Met Thr Val Leu Ala Val
 35 145 150 155 160

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	Leu	Pro	Asn	Met	Tyr	Ile	Gly	Thr	Ile	Glu	Tyr	Asp	Pro	Arg	Thr	Tyr	
					165					170					175		
	Thr	Cys	Ile	Phe	Asn	Tyr	Leu	Asn	Asn	Pro	Val	Phe	Thr	Val	Thr	Ile	
				180					185					190			
5	Val	Cys	Ile	His	Phe	Val	Leu	Pro	Leu	Leu	Ile	Val	Gly	Phe	Cys	Tyr	
			195					200					205				
	Val	Arg	Ile	Trp	Thr	Lys	Val	Leu	Ala	Ala	Arg	Asp	Pro	Ala	Gly	Gln	
		210					215					220					
10	Asn	Pro	Asp	Asn	Gln	Leu	Ala	Glu	Val	Arg	Asn	Lys	Leu	Thr	Met	Phe	
	225					230					235					240	
	Val	Ile	Phe	Leu	Leu	Phe	Ala	Val	Cys	Trp	Cys	Pro	Ile	Asn	Val	Leu	
				245						250					255		
	Thr	Val	Leu	Val	Ala	Val	Ser	Pro	Lys	Glu	Met	Ala	Gly	Lys	Ile	Pro	
				260					265					270			
15	Asn	Trp	Leu	Tyr	Leu	Ala	Ala	Tyr	Phe	Ile	Ala	Tyr	Phe	Asn	Ser	Cys	
			275					280					285				
	Leu	Asn	Ala	Val	Ile	Tyr	Gly	Leu	Leu	Asn	Glu	Asn	Phe	Arg	Arg	Glu	
		290					295					300					
20	Tyr	Trp	Thr	Ile	Phe	His	Ala	Met	Arg	His	Pro	Ile	Ile	Phe	Phe	Ser	
	305					310					315					320	
	Gly	Leu	Ile	Ser	Asp	Ile	Arg	Glu	Met	Gln	Glu	Ala	Arg	Thr	Leu	Ala	
				325						330					335		
	Arg	Ala	Arg	Ala	His	Ala	Arg	Asp	Gln	Ala	Arg	Glu	Gln	Asp	Arg	Ala	
				340				345						350			
25	His	Ala	Cys	Pro	Ala	Val	Glu	Glu	Thr	Pro	Met	Asn	Val	Arg	Asn	Val	
			355					360					365				
	Pro	Leu	Pro	Gly	Asp	Ala	Ala	Ala	Gly	His	Pro	Asp	Arg	Ala	Ser	Gly	
		370					375					380					
30	His	Pro	Lys	Pro	His	Ser	Arg	Ser	Ser	Ser	Ala	Tyr	Arg	Lys	Ser	Ala	
	385					390					395					400	
	Ser	Thr	His	His	Lys	Ser	Val	Phe	Ser	His	Ser	Lys	Ala	Ala	Ser	Gly	
					405					410					415		
	His	Leu	Lys	Pro	Val	Ser	Gly	His	Ser	Lys	Pro	Ala	Ser	Gly	His	Pro	
			420						425					430			
35	Lys	Ser	Ala	Thr	Val	Tyr	Pro	Lys	Pro	Ala	Ser	Val	His	Phe	Lys	Ala	
			435					440					445				
	Asp	Ser	Val	His	Phe	Lys	Gly	Asp	Ser	Val	His	Phe	Lys	Pro	Asp	Ser	

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	450	455	460
	Val His Phe Lys Pro Ala Ser Ser Asn Pro Lys Pro Ile Thr Gly His		
	465	470	475 480
5	His Val Ser Ala Gly Ser His Ser Lys Ser Ala Phe Asn Ala Ala Thr		
		485 490	495
	Ser His Pro Lys Pro Ile Lys Pro Ala Thr Ser His Ala Glu Pro Thr		
		500 505	510
	Thr Ala Asp Tyr Pro Lys Pro Ala Thr Thr Ser His Pro Lys Pro Ala		
		515 520	525
10	Ala Ala Asp Asn Pro Glu Leu Ser Ala Ser His Cys Pro Glu Ile Pro		
		530 535	540
	Ala Ile Ala His Pro Val Ser Asp Asp Ser Asp Leu Pro Glu Ser Ala		
		545 550	555 560
15	Ser Ser Pro Ala Ala Gly Pro Thr Lys Pro Ala Ala Ser Gln Leu Glu		
		565 570	575
	Ser Asp Thr Ile Ala Asp Leu Pro Asp Pro Thr Val Val Thr Thr Ser		
		580 585	590
	Thr Asn Asp Tyr His Asp Val Val Val Val Asp Val Glu Asp Asp Pro		
		595 600	605
20	Asp Glu Met Ala Val		
		610	

(218) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1854 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

30	ATGGGGCCCA CCCTAGCGGT TCCCACCCC TATGGCTGTA TTGGCTGTAA GCTACCCAG	60
	CCAGAATACC CACCGGCTCT AATCATCTTT ATGTTCTGCG CGATGGTTAT CACCATCGTT	120
	GTAGACCTAA TCGGCAACTC CATGGTCATT TTGGCTGTGA CGAAGAACAA GAAGCTCCGG	180
	AATTCTGGCA ACATCTTCGT GGTCACTCTC TCTGTGGCCG ATATGCTGGT GGCCATCTAC	240
	CCATACCCCTT TGATGCTGCA TGCCATGTCC ATTGGGGGCT GGGATCTGAG CCAGTTACAG	300
35	TGCCAGATGG TCGGGTTCAT CACAGGGCTG AGTGTGGTCG GCTCCATCTT CAACATCGTG	360

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GCAATCGCTA TCAACCGTTA CTGCTACATC TGCCACAGCC TCCAGTACGA ACGGATCTTC 420
AGTGTGCGCA ATACCTGCAT CTACCTGGTC ATCACCTGGA TCATGACCGT CCTGGCTGTC 480
CTGCCCCAACA TGTACATTGG CACCATCGAG TACGATCCTC GCACCTACAC CTGCATCTTC 540
AACTATCTGA ACAACCCTGT CTTCACTGTT ACCATCGTCT GCATCCACTT CGTCCTCCCT 600
5 CTCTCATCG TGGGTTTCTG CTACGTGAGG ATCTGGACCA AAGTGCTGGC GGCCCGTGAC 660
CCTGCAGGGC AGAATCCTGA CAACCAACTT GCTGAGGTTC GCAATAAACT AACCATGTTT 720
GTGATCTTCC TCCTCTTTC AGTGTGCTGG TGCCCTATCA ACGTGCTCAC TGTCTTGGTG 780
GCTGTCAGTC CGAAGGAGAT GGCAGGCAAG ATCCCCAACT GGCTTTATCT TGCAGCCTAC 840
TTCATAGCCT ACTTCAACAG CTGCCTCAAC GCTGTGATCT ACGGGCTCCT CAATGAGAAT 900
10 TTCCGAAGAG AATACTGGAC CATCTTCCAT GCTATGCGGC ACCCTATCAT ATTCTTCTCT 960
GGCCTCATCA GTGATATTCG TGAGATGCAG GAGGCCCGTA CCCTGGCCCG CGCCCGTGCC 1020
CATGCTCGCG ACCAAGCTCG TGAACAAGAC CGTGCCCATG CCTGTCTCTG TGTGGAGGAA 1080
ACCCCGATGA ATGTCCGAA TGTTCCATTA CCTGGTGATG CTGCAGCTGG CCACCCCGAC 1140
CGTGCTCTG GCCACCCTAA GCCCCATTCC AGATCCTCCT CTGCCTATCG CAAATCTGCC 1200
15 TCTACCCACC ACAAGTCTGT CTTTAGCCAC TCCAAGGCTG CCTCTGGTCA CCTCAAGCCT 1260
GTCTCTGGCC ACTCCAAGCC TGCCTCTGGT CACCCCAAGT CTGCCACTGT CTACCCTAAG 1320
CCTGCCTCTG TCATTTCAA GGCTGACTCT GTCCATTTC AAGGTGACTC TGTCCATTTC 1380
AAGCCTGACT CTGTTTCAAT CAAGCCTGCT TCCAGCAACC CCAAGCCCAT CACTGGCCAC 1440
CATGTCTCTG CTGGCAGCCA CTCCAAGTCT GCCTTCAGTG CTGCCACCAG CCACCCTAAA 1500
20 CCCACCACTG GCCACATCAA GCCAGCTACC AGCCATGCTG AGCCCACCAC TGCTGACTAT 1560
CCCAAGCCTG CCACTACCAG CCACCCTAAG CCCACTGCTG CTGACAACCC TGAGCTCTCT 1620
GCCTCCCAT GCCCCGAGAT CCCTGCCATT GCCCACCCTG TGTCTGACGA CAGTGACCTC 1680
CCTGAGTCGG CCTCTAGCCC TGCCGCTGGG CCCACCAAGC CTGCTGCCAG CCAGCTGGAG 1740
TCTGACACCA TCGCTGACCT TCCTGACCCT ACTGTAGTCA CTACCAGTAC CAATGATTAC 1800
25 CATGATGTCG TGGTTGTTGA TGTTGAAGAT GATCCTGATG AAATGGCTGT GTGA 1854

(219) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 617 amino acids

(B) TYPE: amino acid

180

(C) STRANDEDNESS:

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

5 Met Gly Pro Thr Leu Ala Val Pro Thr Pro Tyr Gly Cys Ile Gly Cys
 1 5 10 15
 Lys Leu Pro Gln Pro Glu Tyr Pro Pro Ala Leu Ile Ile Phe Met Phe
 20 25 30
 10 Cys Ala Met Val Ile Thr Ile Val Val Asp Leu Ile Gly Asn Ser Met
 35 40 45
 Val Ile Leu Ala Val Thr Lys Asn Lys Lys Leu Arg Asn Ser Gly Asn
 50 55 60
 Ile Phe Val Val Ser Leu Ser Val Ala Asp Met Leu Val Ala Ile Tyr
 65 70 75 80
 15 Pro Tyr Pro Leu Met Leu His Ala Met Ser Ile Gly Gly Trp Asp Leu
 85 90 95
 Ser Gln Leu Gln Cys Gln Met Val Gly Phe Ile Thr Gly Leu Ser Val
 100 105 110
 20 Val Gly Ser Ile Phe Asn Ile Val Ala Ile Ala Ile Asn Arg Tyr Cys
 115 120 125
 Tyr Ile Cys His Ser Leu Gln Tyr Glu Arg Ile Phe Ser Val Arg Asn
 130 135 140
 Thr Cys Ile Tyr Leu Val Ile Thr Trp Ile Met Thr Val Leu Ala Val
 145 150 155 160
 25 Leu Pro Asn Met Tyr Ile Gly Thr Ile Glu Tyr Asp Pro Arg Thr Tyr
 165 170 175
 Thr Cys Ile Phe Asn Tyr Leu Asn Asn Pro Val Phe Thr Val Thr Ile
 180 185 190
 30 Val Cys Ile His Phe Val Leu Pro Leu Leu Ile Val Gly Phe Cys Tyr
 195 200 205
 Val Arg Ile Trp Thr Lys Val Leu Ala Ala Arg Asp Pro Ala Gly Gln
 210 215 220
 Asn Pro Asp Asn Gln Leu Ala Glu Val Arg Asn Lys Leu Thr Met Phe
 225 230 235 240
 35 Val Ile Phe Leu Leu Phe Ala Val Cys Trp Cys Pro Ile Asn Val Leu
 245 250 255

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	Thr	Val	Leu	Val	Ala	Val	Ser	Pro	Lys	Glu	Met	Ala	Gly	Lys	Ile	Pro	
				260					265					270			
	Asn	Trp	Leu	Tyr	Leu	Ala	Ala	Tyr	Phe	Ile	Ala	Tyr	Phe	Asn	Ser	Cys	
			275					280					285				
5	Leu	Asn	Ala	Val	Ile	Tyr	Gly	Leu	Leu	Asn	Glu	Asn	Phe	Arg	Arg	Glu	
			290				295					300					
	Tyr	Trp	Thr	Ile	Phe	His	Ala	Met	Arg	His	Pro	Ile	Ile	Phe	Phe	Ser	
	305					310					315					320	
10	Gly	Leu	Ile	Ser	Asp	Ile	Arg	Glu	Met	Gln	Glu	Ala	Arg	Thr	Leu	Ala	
					325					330					335		
	Arg	Ala	Arg	Ala	His	Ala	Arg	Asp	Gln	Ala	Arg	Glu	Gln	Asp	Arg	Ala	
				340					345					350			
	His	Ala	Cys	Pro	Ala	Val	Glu	Glu	Thr	Pro	Met	Asn	Val	Arg	Asn	Val	
			355					360					365				
15	Pro	Leu	Pro	Gly	Asp	Ala	Ala	Ala	Gly	His	Pro	Asp	Arg	Ala	Ser	Gly	
			370			375						380					
	His	Pro	Lys	Pro	His	Ser	Arg	Ser	Ser	Ser	Ala	Tyr	Arg	Lys	Ser	Ala	
	385					390					395					400	
20	Ser	Thr	His	His	Lys	Ser	Val	Phe	Ser	His	Ser	Lys	Ala	Ala	Ser	Gly	
				405					410						415		
	His	Leu	Lys	Pro	Val	Ser	Gly	His	Ser	Lys	Pro	Ala	Ser	Gly	His	Pro	
			420					425						430			
	Lys	Ser	Ala	Thr	Val	Tyr	Pro	Lys	Pro	Ala	Ser	Val	His	Phe	Lys	Ala	
			435				440						445				
25	Asp	Ser	Val	His	Phe	Lys	Gly	Asp	Ser	Val	His	Phe	Lys	Pro	Asp	Ser	
			450				455					460					
	Val	His	Phe	Lys	Pro	Ala	Ser	Ser	Asn	Pro	Lys	Pro	Ile	Thr	Gly	His	
	465				470					475					480		
30	His	Val	Ser	Ala	Gly	Ser	His	Ser	Lys	Ser	Ala	Phe	Ser	Ala	Ala	Thr	
				485					490						495		
	Ser	His	Pro	Lys	Pro	Thr	Thr	Gly	His	Ile	Lys	Pro	Ala	Thr	Ser	His	
				500				505					510				
	Ala	Glu	Pro	Thr	Thr	Ala	Asp	Tyr	Pro	Lys	Pro	Ala	Thr	Thr	Ser	His	
			515				520						525				
35	Pro	Lys	Pro	Thr	Ala	Ala	Asp	Asn	Pro	Glu	Leu	Ser	Ala	Ser	His	Cys	
			530				535					540					
	Pro	Glu	Ile	Pro	Ala	Ile	Ala	His	Pro	Val	Ser	Asp	Asp	Ser	Asp	Leu	

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[illegible]

10 (220) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1548 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

	ATGGGACATA	ACGGGAGCTG	GATCTCTCCA	AATGCCAGCG	AGCCGCACAA	CGCGTCCGGC	60
	GCCGAGGCTG	CGGGTGTGAA	CCGCAGCGCG	CTCGGGGAGT	TCGGCGAGGC	GCAGCTGTAC	120
20	CGCCAGTTCA	CCACCACCGT	GCAGGTCGTC	ATCTTCATAG	GCTCGCTGCT	CGGAAACTTC	180
	ATGGTGTTAT	GGTCAACTTG	CCGCACAACC	GTGTTCAAAT	CTGTCACCAA	CAGGTTTCAT	240
	AAAAACCTGG	CCTGCTCGGG	GATTTGTGCC	AGCCTGGTCT	GTGTGCCCTT	CGACATCATC	300
	CTCAGCACCA	GTCCTCACTG	TTGCTGGTGG	ATCTACACCA	TGCTCTTCTG	CAAGGTCGTC	360
	AAATTTTTCG	ACAAAGTATT	CTGCTCTGTG	ACCATCCTCA	GCTTCCCTGC	TATTGCTTTG	420
25	GACAGGTA	CTCAGTCCT	CTATCCACTG	GAGAGGAAAA	TATCTGATGC	CAAGTCCCGT	480
	GAACTGGTGA	TGTACATCTG	GGCCCATGCA	GTGGTGGCCA	GTGTCCCTGT	GTTTGCACTA	540
	ACCAATGTGG	CTGACATCTA	TGCCACGTCC	ACCTGCACGG	AAGTCTGGAG	CAACTCCTTG	600
	GGCCACCTGG	TGTACGTTCT	GGTGTATAAC	ATCACCACGG	TCATTGTGCC	TGTGGTGGTG	660
	GTGTTCTCT	TCTTGATACT	GATCCGACGG	GCCCTGAGTG	CCAGCCAGAA	GAAGAAGGTC	720
30	ATCATAGCAG	CGCTCCGGAC	CCCACAGAAC	ACCATCTCTA	TTCCCTATGC	CTCCCAGCGG	780
	GAGGCCGAGC	TGAAAGCCAC	CCTGCTCTCC	ATGGTGATGG	TCTTCATCTT	GTGTAGCGTG	840
	CCCTATGCCA	CCCTGGTCGT	CTACCAGACT	GTGCTCAATG	TCCCTGACAC	TTCCGTCTTC	900

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TTGCTGCTCA CTGCTGTTTG GCTGCCCAAA GTCTCCCTGC TGGCAAACCC TGTTCTCTTT 960
 CTTACTGTGA ACAAATCTGT CCGCAAGTGC TTGATAGGGA CCCTGGTGCA ACTACACCAC 1020
 CGGTACAGTC GCCGTAATGT GGTCAGTACA GGGAGTGGCA TGGCTGAGGC CAGCCTGGAA 1080
 CCCAGCATAC GCTCGGGTAG CCAGCTCCTG GAGATGTTCC ACATTGGGCA GCAGCAGATC 1140
 5 TTTAAGCCCA CAGAGGATGA GGAAGAGAGT GAGGCCAAGT ACATTGGGCTC AGCTGACTTC 1200
 CAGGCCAAGG AGATATTTAG CACCTGCCTG GAGGGAGAGC AGGGGCCACA GTTTGCGCCC 1260
 TCTGCCCCAC CCCTGAGCAC AGTGGACTCT GTATCCCAGG TGGCACCGGC AGCCCCTGTG 1320
 GAACCTGAAA CATTCCCTGA TAAGTATTCC CTGCAGTTTG GCTTTGGGCC TTTTGAGTTG 1380
 CCTCCTCAGT GGCTCTCAGA GACCCGAAAC AGCAAGAAGC GGCTGCTTCC CCCCTTGGGC 1440
 10 AACACCCCAG AAGAGCTGAT CCAGACAAAG GTGCCCAAGG TAGGCAGGCT GGAGCGGAAG 1500
 ATGAGCAGAA ACAATAAAGT GAGCATTTTT CCAAAGGTGG ATTCCTAG 1548

(221) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 515 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

20 Met Gly His Asn Gly Ser Trp Ile Ser Pro Asn Ala Ser Glu Pro His
 1 5 10 15
 Asn Ala Ser Gly Ala Glu Ala Ala Gly Val Asn Arg Ser Ala Leu Gly
 20 25 30
 25 Glu Phe Gly Glu Ala Gln Leu Tyr Arg Gln Phe Thr Thr Thr Val Gln
 35 40 45
 Val Val Ile Phe Ile Gly Ser Leu Leu Gly Asn Phe Met Val Leu Trp
 50 55 60
 Ser Thr Cys Arg Thr Thr Val Phe Lys Ser Val Thr Asn Arg Phe Ile
 65 70 75 80
 30 Lys Asn Leu Ala Cys Ser Gly Ile Cys Ala Ser Leu Val Cys Val Pro
 85 90 95
 Phe Asp Ile Ile Leu Ser Thr Ser Pro His Cys Cys Trp Trp Ile Tyr
 100 105 110

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	Thr	Met	Leu	Phe	Cys	Lys	Val	Val	Lys	Phe	Leu	His	Lys	Val	Phe	Cys	
			115						120					125			
	Ser	Val	Thr	Ile	Leu	Ser	Phe	Pro	Ala	Ile	Ala	Leu	Asp	Arg	Tyr	Tyr	
		130					135					140					
5	Ser	Val	Leu	Tyr	Pro	Leu	Glu	Arg	Lys	Ile	Ser	Asp	Ala	Lys	Ser	Arg	
	145					150					155					160	
	Glu	Leu	Val	Met	Tyr	Ile	Trp	Ala	His	Ala	Val	Val	Ala	Ser	Val	Pro	
					165					170					175		
10	Val	Phe	Ala	Val	Thr	Asn	Val	Ala	Asp	Ile	Tyr	Ala	Thr	Ser	Thr	Cys	
				180					185					190			
	Thr	Glu	Val	Trp	Ser	Asn	Ser	Leu	Gly	His	Leu	Val	Tyr	Val	Leu	Val	
			195					200					205				
	Tyr	Asn	Ile	Thr	Thr	Val	Ile	Val	Pro	Val	Val	Val	Val	Phe	Leu	Phe	
		210					215						220				
15	Leu	Ile	Leu	Ile	Arg	Arg	Ala	Leu	Ser	Ala	Ser	Gln	Lys	Lys	Lys	Val	
	225					230					235					240	
	Ile	Ile	Ala	Ala	Leu	Arg	Thr	Pro	Gln	Asn	Thr	Ile	Ser	Ile	Pro	Tyr	
					245					250					255		
20	Ala	Ser	Gln	Arg	Glu	Ala	Glu	Leu	Lys	Ala	Thr	Leu	Leu	Ser	Met	Val	
				260					265					270			
	Met	Val	Phe	Ile	Leu	Cys	Ser	Val	Pro	Tyr	Ala	Thr	Leu	Val	Val	Tyr	
			275					280					285				
	Gln	Thr	Val	Leu	Asn	Val	Pro	Asp	Thr	Ser	Val	Phe	Leu	Leu	Leu	Thr	
		290					295					300					
25	Ala	Val	Trp	Leu	Pro	Lys	Val	Ser	Leu	Leu	Ala	Asn	Pro	Val	Leu	Phe	
	305					310					315					320	
	Leu	Thr	Val	Asn	Lys	Ser	Val	Arg	Lys	Cys	Leu	Ile	Gly	Thr	Leu	Val	
				325						330					335		
30	Gln	Leu	His	His	Arg	Tyr	Ser	Arg	Arg	Asn	Val	Val	Ser	Thr	Gly	Ser	
				340					345					350			
	Gly	Met	Ala	Glu	Ala	Ser	Leu	Glu	Pro	Ser	Ile	Arg	Ser	Gly	Ser	Gln	
		355						360					365				
	Leu	Leu	Glu	Met	Phe	His	Ile	Gly	Gln	Gln	Gln	Ile	Phe	Lys	Pro	Thr	
		370					375					380					
35	Glu	Asp	Glu	Glu	Glu	Ser	Glu	Ala	Lys	Tyr	Ile	Gly	Ser	Ala	Asp	Phe	
	385					390					395					400	
	Gln	Ala	Lys	Glu	Ile	Phe	Ser	Thr	Cys	Leu	Glu	Gly	Glu	Gln	Gly	Pro	

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		405		410		415
	Gln Phe Ala Pro Ser Ala Pro Pro Leu Ser Thr Val Asp Ser Val Ser					
		420		425		430
5	Gln Val Ala Pro Ala Ala Pro Val Glu Pro Glu Thr Phe Pro Asp Lys					
		435		440		445
	Tyr Ser Leu Gln Phe Gly Phe Gly Pro Phe Glu Leu Pro Pro Gln Trp					
		450		455		460
	Leu Ser Glu Thr Arg Asn Ser Lys Lys Arg Leu Leu Pro Pro Leu Gly					
		465		470		475
10	Asn Thr Pro Glu Glu Leu Ile Gln Thr Lys Val Pro Lys Val Gly Arg					
		485		490		495
	Val Glu Arg Lys Met Ser Arg Asn Asn Lys Val Ser Ile Phe Pro Lys					
		500		505		510
15	Val Asp Ser					
		515				

(222) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1164 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

	ATGAATCGGC ACCATCTGCA GGATCACTTT CTGGAAATAG ACAAGAAGAA CTGCTGTGTG	60
25	TTCCGAGATG ACTTCATTGC CAAGGTGTTG CCGCCGGTGT TGGGGCTGGA GTTTATCTTT	120
	GGGCTTCTGG GCAATGGCCT TGCCCTGTGG ATTTTCTGTT TCCACCTCAA GTCCTGGAAA	180
	TCCAGCCGGA TTTTCCTGTT CAACCTGGCA GTAGCTGACT TTCTACTGAT CATCTGCCTG	240
	CCGTTTCGTGA TGGACTACTA TGTGCGGCGT TCAGACTGGA AGTTTGGGGA CATCCCTTGC	300
	CGGCTGGTGC TCTTCATGTT TGCCATGAAC CGCCAGGGCA GCATCATCTT CCTCACGGTG	360
30	GTGGCGGTAG ACAGGTATTT CCGGGTGGTC CATCCCCACC ACGCCCTGAA CAAGATCTCC	420
	AATGGACAG CAGCCATCAT CTCTTGCCTT CTGTGGGGCA TCACTGTTGG CCTAACAGTC	480
	CACCTCCTGA AGAAGAAGTT GCTGATCCAG AATGGCCCTG CAAATGTGTG CATCAGCTTC	540
	AGCATCTGCC ATACCTTCCG GTGGCACGAA GCTATGTTCC TCCTGGAGTT CCTCCTGCCC	600

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CTGGGCATCA TCCTGTTCTG CTCAGCCAGA ATTATCTGGA GCCTGCGGCA GAGACAAATG 660
 GACCGGCATG CCAAGATCAA GAGAGCCAAA ACCTTCATCA TGGTGGTGGC CATCGTCTTT 720
 GTCATCTGCT TCCTTCCCAG CGTGGTTGTG CGGATCCGCA TCTTCTGGCT CCTGCACACT 780
 TCGGGCACGC AGAATTGTGA AGTGTACCGC TCGGTGGACC TGGCGTTCTT TATCACTCTC 840
 5 AGCTTCACCT ACATGAACAG CATGCTGGAC CCCGTGGTGT ACTACTTCTC CAGCCCATCC 900
 TTTCCCAACT TCTTCTCCAC TTTGATCAAC CGCTGCCTCC AGAGGAAGAT GACAGGTGAG 960
 CCAGATAATA ACCGCAGCAC GAGCGTCGAG CTCACAGGGG ACCCCAACAA AACCAGAGGC 1020
 GCTCCAGAGG CGTTAATGGC CAACTCCGGT GAGCCATGGA GCCCCTCTTA TCTGGGCCCA 1080
 ACCTCAAATA ACCATTCCAA GAAGGGACAT TGTCACCAAG AACCAGCATC TCTGGAGAAA 1140
 10 CAGTTGGGCT GTTGCATCGA GTAA 1164

(223) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 387 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

20 Met Asn Arg His His Leu Gln Asp His Phe Leu Glu Ile Asp Lys Lys
 1 5 10 15
 Asn Cys Cys Val Phe Arg Asp Asp Phe Ile Ala Lys Val Leu Pro Pro
 20 25 30
 Val Leu Gly Leu Glu Phe Ile Phe Gly Leu Leu Gly Asn Gly Leu Ala
 35 40 45
 25 Leu Trp Ile Phe Cys Phe His Leu Lys Ser Trp Lys Ser Ser Arg Ile
 50 55 60
 Phe Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu Ile Ile Cys Leu
 65 70 75 80
 30 Pro Phe Val Met Asp Tyr Tyr Val Arg Arg Ser Asp Trp Lys Phe Gly
 85 90 95
 Asp Ile Pro Cys Arg Leu Val Leu Phe Met Phe Ala Met Asn Arg Gln
 100 105 110
 Gly Ser Ile Ile Phe Leu Thr Val Val Ala Val Asp Arg Tyr Phe Arg
 115 120 125

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Val Val His Pro His His Ala Leu Asn Lys Ile Ser Asn Trp Thr Ala
130 135 140

Ala Ile Ile Ser Cys Leu Leu Trp Gly Ile Thr Val Gly Leu Thr Val
145 150 155 160

5 His Leu Leu Lys Lys Lys Leu Leu Ile Gln Asn Gly Pro Ala Asn Val
165 170 175

Cys Ile Ser Phe Ser Ile Cys His Thr Phe Arg Trp His Glu Ala Met
180 185 190

10 Phe Leu Leu Glu Phe Leu Leu Pro Leu Gly Ile Ile Leu Phe Cys Ser
195 200 205

Ala Arg Ile Ile Trp Ser Leu Arg Gln Arg Gln Met Asp Arg His Ala
210 215 220

Lys Ile Lys Arg Ala Lys Thr Phe Ile Met Val Val Ala Ile Val Phe
225 230 235 240

15 Val Ile Cys Phe Leu Pro Ser Val Val Val Arg Ile Arg Ile Phe Trp
245 250 255

Leu Leu His Thr Ser Gly Thr Gln Asn Cys Glu Val Tyr Arg Ser Val
260 265 270

20 Asp Leu Ala Phe Phe Ile Thr Leu Ser Phe Thr Tyr Met Asn Ser Met
275 280 285

Leu Asp Pro Val Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Asn Phe
290 295 300

Phe Ser Thr Leu Ile Asn Arg Cys Leu Gln Arg Lys Met Thr Gly Glu
305 310 315 320

25 Pro Asp Asn Asn Arg Ser Thr Ser Val Glu Leu Thr Gly Asp Pro Asn
325 330 335

Lys Thr Arg Gly Ala Pro Glu Ala Leu Met Ala Asn Ser Gly Glu Pro
340 345 350

30 Trp Ser Pro Ser Tyr Leu Gly Pro Thr Ser Asn Asn His Ser Lys Lys
355 360 365

Gly His Cys His Gln Glu Pro Ala Ser Leu Glu Lys Gln Leu Gly Cys
370 375 380

Cys Ile Glu
385

35 (224) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1212 base pairs

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(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: DNA (genomic)

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

	ATGGCTTGCA ATGGCAGTGC GGCCAGGGGG CACTTTGACC CTGAGGACTT GAACCTGACT	60
	GACGAGGCAC TGAGACTCAA GTACCTGGGG CCCCAGCAGA CAGAGCTGTT CATGCCCATC	120
	TGTGCCACAT ACCTGCTGAT CTTCTGTGGT GGCCTGTGGT GCAATGGGCT GACCTGTCTG	180
	GTATCCTGTC GCCACAAGGC CATGCGCAGC CCTACCAACT ACTACCTCTT CAGCCTGGCC	240
10	GTGTCGGACC TGCTGGTGCT GCTGGTGGGC CTGCCCCCTG AGCTCTATGA GATGTGGCAC	300
	AACTACCCCT TCCTGCTGGG CGTTGGTGGC TGCTATTTCC GCACGCTACT GTTTGAGATG	360
	GTCTGCCTGG CCTCAGTGCT CAACGTCACT GCCCTGAGCG TGAACGCTA TGTGGCCGTG	420
	GTGCACCCAC TCCAGGCCAG GTCCATGGTG ACGCGGGCCC ATGTGCGCCG AGTGCTTGGG	480
	GCCGTCTGGG GTCTTGCCAT GCTCTGCTCC CTGCCAACA CCAGCCTGCA CGGCATCCGG	540
15	CAGTGCACG TGCCCTGCCG GGGCCAGTG CCAGACTCAG CTGTTTGCAT GCTGGTCCGC	600
	CCACGGGCCC TCTACAACAT GGTAGTGCA ACCACCGCGC TGCTCTTCTT CTGCCTGCCC	660
	ATGGCCATCA TGAGCGTGCT CTACCTGCTC ATTGGGCTGC GACTGCGGCG GGAGAGGCTG	720
	CTGCTCATGC AGGAGGCCAA GGGCAGGGGC TCTGCAGCAG CCAGGTCCAG ATACACCTGC	780
	AGGCTCCAGC AGCAGATCG GGGCCGAGG CAAGTGAAGA AGATGCTGTT TGTCTTGGTC	840
20	GTGGTGTTTG GCATCTGCTG GGCCCCGTTC CACGCCGACC GCGTCATGTG GAGCGTCGTG	900
	TCACAGTGGA CAGATGGCCT GCACCTGGCC TTCCAGCACG TGCACGTCAT CTCCGGCATC	960
	TTCTTCTACC TGGGCTCGGC GGCCAACCCC GTGCTCTATA GCCTCATGTC CAGCCGCTTC	1020
	CGAGAGACCT TCCAGGAGGC CCTGTGCCTC GGGGCCTGCT GCCATCGCCT CAGACCCCGC	1080
	CACAGCTCCC ACAGCCTCAG CAGGATGACC ACAGGCAGCA CCCTGTGTGA TGTGGGCTCC	1140
25	CTGGGCAGCT GGGTCCACCC CCTGGCTGGG AACGATGGCC CAGAGGCGCA GCAAGAGACC	1200
	GATCCATCCT GA	1212

(225) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 403 amino acids
(B) TYPE: amino acid

30

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(C) STRANDEDNESS:

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

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5  Met Ala Cys Asn Gly Ser Ala Ala Arg Gly His Phe Asp Pro Glu Asp
   1           5           10           15

   Leu Asn Leu Thr Asp Glu Ala Leu Arg Leu Lys Tyr Leu Gly Pro Gln
      20           25           30

10  Gln Thr Glu Leu Phe Met Pro Ile Cys Ala Thr Tyr Leu Leu Ile Phe
      35           40           45

   Val Val Gly Ala Val Gly Asn Gly Leu Thr Cys Leu Val Ile Leu Arg
      50           55           60

   His Lys Ala Met Arg Thr Pro Thr Asn Tyr Tyr Leu Phe Ser Leu Ala
   65           70           75           80

15  Val Ser Asp Leu Leu Val Leu Leu Val Gly Leu Pro Leu Glu Leu Tyr
      85           90           95

   Glu Met Trp His Asn Tyr Pro Phe Leu Leu Gly Val Gly Gly Cys Tyr
      100          105          110

   Phe Arg Thr Leu Leu Phe Glu Met Val Cys Leu Ala Ser Val Leu Asn
   115          120          125

20  Val Thr Ala Leu Ser Val Glu Arg Tyr Val Ala Val Val His Pro Leu
      130          135          140

   Gln Ala Arg Ser Met Val Thr Arg Ala His Val Arg Arg Val Leu Gly
   145          150          155          160

25  Ala Val Trp Gly Leu Ala Met Leu Cys Ser Leu Pro Asn Thr Ser Leu
      165          170          175

   His Gly Ile Arg Gln Leu His Val Pro Cys Arg Gly Pro Val Pro Asp
      180          185          190

   Ser Ala Val Cys Met Leu Val Arg Pro Arg Ala Leu Tyr Asn Met Val
   195          200          205

30  Val Gln Thr Thr Ala Leu Leu Phe Phe Cys Leu Pro Met Ala Ile Met
      210          215          220

   Ser Val Leu Tyr Leu Leu Ile Gly Leu Arg Leu Arg Arg Glu Arg Leu
   225          230          235          240

35  Leu Leu Met Gln Glu Ala Lys Gly Arg Gly Ser Ala Ala Ala Arg Ser
      245          250          255

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Arg Tyr Thr Cys Arg Leu Gln Gln His Asp Arg Gly Arg Arg Gln Val
 260 265 270
 Lys Lys Met Leu Phe Val Leu Val Val Val Phe Gly Ile Cys Trp Ala
 275 280 285
 5 Pro Phe His Ala Asp Arg Val Met Trp Ser Val Val Ser Gln Trp Thr
 290 295 300
 Asp Gly Leu His Leu Ala Phe Gln His Val His Val Ile Ser Gly Ile
 305 310 315 320
 10 Phe Phe Tyr Leu Gly Ser Ala Ala Asn Pro Val Leu Tyr Ser Leu Met
 325 330 335
 Ser Ser Arg Phe Arg Glu Thr Phe Gln Glu Ala Leu Cys Leu Gly Ala
 340 345 350
 Cys Cys His Arg Leu Arg Pro Arg His Ser Ser His Ser Leu Ser Arg
 355 360 365
 15 Met Thr Thr Gly Ser Thr Leu Cys Asp Val Gly Ser Leu Gly Ser Trp
 370 375 380
 Val His Pro Leu Ala Gly Asn Asp Gly Pro Glu Ala Gln Gln Glu Thr
 385 390 395 400
 20 Asp Pro Ser
 (226) INFORMATION FOR SEQ ID NO:225:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1098 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:
 ATGGGGAACA TCACTGCAGA CAACTCCTCG ATGAGCTGTA CCATCGACCA TACCATCCAC 60
 30 CAGACGCTGG CCCCGGTGGT CTATGTTACC GTGCTGGTGG TGGGCTTCCC GGCCAACTGC 120
 CTGTCCCTCT ACTTCGGCTA CCTGCAGATC AAGGCCCGGA ACGAGCTGGG CGTGTACCTG 180
 TGCAACCTGA CGGTGGCCGA CCTCTTCTAC ATCTGCTCGC TGCCCTTCTG GCTGCAGTAC 240
 GTGCTGCAGC ACGACAACTG GTCTCACGGC GACCTGTCCT GCCAGGTGTG CGGCATCCTC 300
 CTGTACGAGA ACATCTACAT CAGCGTGGGC TTCCTCTGCT GCATCTCCGT GGACCGCTAC 360
 35 CTGGCTGTGG CCCATCCCTT CCGCTCCAC CAGTCCGGA CCCTGAAGGC GGCCGTCGGC 420

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GTCAGCGTGG TCATCTGGGC CAAGGAGCTG CTGACCAGCA TCTACTTCCT GATGCACGAG 480
 GAGGTCATCG AGGACGAGAA CCAGCACCGC GTGTGCTTTG AGCACTACCC CATCCAGGCA 540
 TGGCAGCGCG CCATCAACTA CTACCGCTTC CTGGTGGGCT TCCTCTTCCC CATCTGCCTG 600
 CTGCTGGCGT CCTACCAGGG CATCCTGCGC GCCGTGCGCC GGAGCCACGG CACCCAGAAG 660
 5 AGCCGCAAGG ACCAGATCAA GCGGCTGGTG CTCAGACCG TGGTCATCTT CCTGGCCTGC 720
 TTCCTGCCCT ACCACGTGTT GCTGCTGGTG CGCAGCGTCT GGGAGGCCAG CTGCGACTTC 780
 GCCAAGGGCG TTTTCAACGC CTACCACTTC TCCCTCCTGC TCACCAGCTT CAACTGCGTC 840
 GCCGACCCCG TGCTCTACTG CTTCGTCAGC GAGACCACCC ACCGGGACCT GGCCCCGCTC 900
 CGCGGGGCCT GCCTGGCCTT CCTCACCTGC TCCAGGACCG GCCGGGCCAG GGAGGCCTAC 960
 10 CCGCTGGGTG CCCCCGAGGC CTCCGGGAAA AGCGGGGCC AGGGTGAGGA GCCCGAGCTG 1020
 TTGACCAAGC TCCACCCGGC CTTCAGACC CCTAACTCGC CAGGGTCGGG CGGGTTCCCC 1080
 ACGGGCAGGT TGGCCTAG 1098

(227) INFORMATION FOR SEQ ID NO:226:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 365 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

Met Gly Asn Ile Thr Ala Asp Asn Ser Ser Met Ser Cys Thr Ile Asp
 1 5 10 15
 His Thr Ile His Gln Thr Leu Ala Pro Val Val Tyr Val Thr Val Leu
 20 25 30
 25 Val Val Gly Phe Pro Ala Asn Cys Leu Ser Leu Tyr Phe Gly Tyr Leu
 35 40 45
 Gln Ile Lys Ala Arg Asn Glu Leu Gly Val Tyr Leu Cys Asn Leu Thr
 50 55 60
 30 Val Ala Asp Leu Phe Tyr Ile Cys Ser Leu Pro Phe Trp Leu Gln Tyr
 65 70 75 80
 Val Leu Gln His Asp Asn Trp Ser His Gly Asp Leu Ser Cys Gln Val
 85 90 95
 Cys Gly Ile Leu Leu Tyr Glu Asn Ile Tyr Ile Ser Val Gly Phe Leu

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	100	105	110
	Cys Cys Ile Ser Val Asp Arg Tyr Leu Ala Val Ala His Pro Phe Arg		
	115	120	125
5	Phe His Gln Phe Arg Thr Leu Lys Ala Ala Val Gly Val Ser Val Val		
	130	135	140
	Ile Trp Ala Lys Glu Leu Leu Thr Ser Ile Tyr Phe Leu Met His Glu		
	145	150	155 160
	Glu Val Ile Glu Asp Glu Asn Gln His Arg Val Cys Phe Glu His Tyr		
	165	170	175
10	Pro Ile Gln Ala Trp Gln Arg Ala Ile Asn Tyr Tyr Arg Phe Leu Val		
	180	185	190
	Gly Phe Leu Phe Pro Ile Cys Leu Leu Leu Ala Ser Tyr Gln Gly Ile		
	195	200	205
15	Leu Arg Ala Val Arg Arg Ser His Gly Thr Gln Lys Ser Arg Lys Asp		
	210	215	220
	Gln Ile Lys Arg Leu Val Leu Ser Thr Val Val Ile Phe Leu Ala Cys		
	225	230	235 240
	Phe Leu Pro Tyr His Val Leu Leu Leu Val Arg Ser Val Trp Glu Ala		
	245	250	255
20	Ser Cys Asp Phe Ala Lys Gly Val Phe Asn Ala Tyr His Phe Ser Leu		
	260	265	270
	Leu Leu Thr Ser Phe Asn Cys Val Ala Asp Pro Val Leu Tyr Cys Phe		
	275	280	285
25	Val Ser Glu Thr Thr His Arg Asp Leu Ala Arg Leu Arg Gly Ala Cys		
	290	295	300
	Leu Ala Phe Leu Thr Cys Ser Arg Thr Gly Arg Ala Arg Glu Ala Tyr		
	305	310	315 320
	Pro Leu Gly Ala Pro Glu Ala Ser Gly Lys Ser Gly Ala Gln Gly Glu		
	325	330	335
30	Glu Pro Glu Leu Leu Thr Lys Leu His Pro Ala Phe Gln Thr Pro Asn		
	340	345	350
	Ser Pro Gly Ser Gly Gly Phe Pro Thr Gly Arg Leu Ala		
	355	360	365

(228) INFORMATION FOR SEQ ID NO:227:

35

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1416 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

5	ATGGATATTC TTTGTGAAGA AAATACTTCT TTGAGCTCAA CTACGAACTC CCTAATGCAA	60
	TTAAATGATG ACAACAGGCT CTACAGTAAT GACTTTAACT CCGGAGAAGC TAACACTTCT	120
	GATGCATTTA ACTGGACAGT CGACTCTGAA AATCGAACCA ACCTTTCCTG TGAAGGGTGC	180
	CTCTCACCGT CGTGTCTCTC CTTACTTCAT CTCCAGGAAA AAAACTGGTC TGCTTTACTG	240
	ACAGCCGTAG TGATTATTCT AACTATTGCT GGAAACATAC TCGTCATCAT GGCAGTGTCC	300
10	CTAGAGAAAA AGCTGCAGAA TGCCACCAAC TATTTCTGA TGTCATTGC CATAGCTGAT	360
	ATGCTGCTGG GTTTCCTTGT CATGCCCGTG TCCATGTTAA CCATCCTGTA TGGGTACCGG	420
	TGGCCTCTGC CGAGCAAGCT TTGTGCAGTC TGGATTACC TGGACGTGCT CTTCTCCACG	480
	GCCTCCATCA TGCACCTCTG CGCCATCTCG CTGGACCGCT ACGTCGCCAT CCAGAATCCC	540
	ATCCACCACA GCCGCTTCAA CTCCAGAACT AAGGCATTTC TGAAAATCAT TGCTGTTTGG	600
15	ACCATATCAG TAGGTATATC CATGCCAATA CCAGTCTTTG GGCTACAGGA CGATTCGAAG	660
	GTCTTTAAGG AGGGGAGTTG CTTACTCGCC GATGATAACT TTGTCCTGAT CGGCTCTTTT	720
	GTGTCATTTT TCATTCCCTT AACCATCATG GTGATCACCT ACTTTCTAAC TATCAAGTCA	780
	CTCCAGAAAG AAGCTACTTT GTGTGTAAGT GATCTTGGCA CACGGGCCAA ATTAGCTTCT	840
	TTCAGCTTCC TCCCTCAGAG TTCTTTGTCT TCAGAAAAGC TCTCCAGCG GTCGATCCAT	900
20	AGGGAGCCAG GGTCTACAC AGGCAGGAGG ACTATGCAGT CCATCAGCAA TGAGCAAAAG	960
	GCAAAGAAGG TGCTGGGCAT CGTCTTCTTC CTGTTTGTGG TGATGTGGTG CCCTTTCTTC	1020
	ATCACAAACA TCATGGCCGT CATCTGCAAA GAGTCCTGCA ATGAGGATGT CATTGGGGCC	1080
	CTGCTCAATG TGTTTGTTTG GATCGGTTAT CTCTCTTCAG CAGTCAACCC ACTAGTCTAC	1140
	ACACTGTTCA ACAAGACCTA TAGGTCAGCC TTTTCACGGT ATATTCAGTG TCAGTACAAG	1200
25	GAAAACAAAA AACCATTGCA GTTAATTTTA GTGAACACAA TACCGGCTTT GGCCTACAAG	1260
	TCTAGCCAAC TTCAAATGGG ACAAAAAAAG AATTCAAAGC AAGATGCCAA GACAACAGAT	1320
	AATGACTGCT CAATGGTTGC TCTAGGAAAG CAGTATTCTG AAGAGGCTTC TAAAGACAAT	1380
	AGCGACGGAG TGAATGAAAA GGTGAGCTGT GTGTGA	1416

(A) LENGTH: 470 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

10	1	Met	Asp	Ile	Leu	Cys	Glu	Glu	Asn	Thr	Ser	Leu	Ser	Ser	Thr	Thr	Asn
				5						10						15	
		Ser	Leu	Met	Gln	Leu	Asn	Asp	Asp	Asn	Arg	Leu	Tyr	Ser	Asn	Asp	Phe
				20					25					30			
		Asn	Ser	Gly	Glu	Ala	Asn	Thr	Ser	Asp	Ala	Phe	Asn	Trp	Thr	Val	Asp
				35					40					45			
15		Ser	Glu	Asn	Arg	Thr	Asn	Leu	Ser	Cys	Glu	Gly	Cys	Leu	Ser	Pro	Ser
			50					55					60				
		Cys	Leu	Ser	Leu	Leu	His	Leu	Gln	Glu	Lys	Asn	Trp	Ser	Ala	Leu	Leu
		65					70					75					80
20		Thr	Ala	Val	Val	Ile	Ile	Leu	Thr	Ile	Ala	Gly	Asn	Ile	Leu	Val	Ile
						85					90					95	
		Met	Ala	Val	Ser	Leu	Glu	Lys	Lys	Leu	Gln	Asn	Ala	Thr	Asn	Tyr	Phe
					100					105					110		
		Leu	Met	Ser	Leu	Ala	Ile	Ala	Asp	Met	Leu	Leu	Gly	Phe	Leu	Val	Met
				115					120					125			
25		Pro	Val	Ser	Met	Leu	Thr	Ile	Leu	Tyr	Gly	Tyr	Arg	Trp	Pro	Leu	Pro
			130					135					140				
		Ser	Lys	Leu	Cys	Ala	Val	Trp	Ile	Tyr	Leu	Asp	Val	Leu	Phe	Ser	Thr
		145					150					155					160
		Ala	Ser	Ile	Met	His	Leu	Cys	Ala	Ile	Ser	Leu	Asp	Arg	Tyr	Val	Ala
					165						170					175	
30		Ile	Gln	Asn	Pro	Ile	His	His	Ser	Arg	Phe	Asn	Ser	Arg	Thr	Lys	Ala
					180					185					190		
		Phe	Leu	Lys	Ile	Ile	Ala	Val	Trp	Thr	Ile	Ser	Val	Gly	Ile	Ser	Met
				195					200					205			
35		Pro	Ile	Pro	Val	Phe	Gly	Leu	Gln	Asp	Asp	Ser	Lys	Val	Phe	Lys	Glu
			210					215					220				
		Gly	Ser	Cys	Leu	Leu	Ala	Asp	Asp	Asn	Phe	Val	Leu	Ile	Gly	Ser	Phe
		225					230					235					240

[illegible]

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1377 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

	ATGGTGAACC TGAGGAATGC GGTGCATTCA TTCCTTGTGC ACCTAATTGG CCTATTGGTT	60
	TGGCAATGTG ATATTTCTGT GAGCCCAGTA GCAGCTATAG TAACTGACAT TTTCAATACC	120
	TCCGATGGTG GACGCTTCAA ATTCCCAGAC GGGGTACAAA ACTGGCCAGC ACTTTCAATC	180
5	GTCATCATAA TAATCATGAC AATAGGTGGC AACATCCTTG TGATCATGGC AGTAAGCATG	240
	GAAAAGAAAC TGCACAATGC CACCAATTAC TTCTTAATGT CCCTAGCCAT TGCTGATATG	300
	CTAGTGGGAC TACTTGTCTAT GCCCCTGTCT CTCCTGGCAA TCCTTTATGA TTATGTCTGG	360
	CCACTACCTA GATATTTGTG CCCCCTCTGG ATTTCTTTAG ATGTTTTATT TTCAACAGCG	420
	TCCATCATGC ACCTCTGCGC TATATCGCTG GATCGGTATG TAGCAATACG TAATCCTATT	480
10	GAGCATAGCC GTTTCAATTC GCGGACTAAG GCCATCATGA AGATTGCTAT TGTTTGGGCA	540
	ATTTCTATAG GTGTATCAGT TCCTATCCCT GTGATTGGAC TGAGGGACGA AGAAAAGGTG	600
	TTCGTGAACA ACACGACGTG CGTGCTCAAC GACCCAAATT TCGTTCTTAT TGGGTCCTTC	660
	GTAGCTTTCT TCATACCGCT GACGATTATG GTGATTACGT ATGTCCTGAC CATCTACGTT	720
	CTGCGCCGAC AAGCTTTGAT GTTACTGCAC GGCCACACCG AGGAACCGCC TGGACTAAGT	780
15	CTGGATTTCC TGAAGTGCTG CAAGAGGAAT ACGGCCGAGG AAGAGAACTC TGCAAACCCT	840
	AACCAAGACC AGAACGCACG CCGAAGAAAG AAGAAGGAGA GACGTCCTAG GGGCACCATG	900
	CAGGCTATCA ACAATGAAAG AAAAGCTAAG AAAGTCCTTG GGATTGTTTT CTTTGTGTTT	960
	CTGATCATGT GGTGCCCATT TTTCATTACC AATATTCTGT CTGTTCTTTG TGAGAAGTCC	1020
	TGTAACCAAA AGCTCATGGA AAAGCTTCTG AATGTGTTTG TTTGGATTGG CTATGTTTGT	1080
20	TCAGGAATCA ATCCTCTGGT GTATACTCTG TTCAACAAAA TTTACCGAAG GGCATTCTCC	1140
	AACTATTTGC GTTGCAATTA TAAGGTAGAG AAAAAGCCTC CTGTCAGGCA GATTCCAAGA	1200
	GTTGCCGCCA CTGCTTTGTC TGGGAGGGAG CTTAATGTTA ACATTATATCG GCATACCAAT	1260
	GAACCGGTGA TCGAGAAAGC CAGTGACAAT GAGCCCGGTA TAGAGATGCA AGTTGAGAAT	1320
	TTAGAGTTAC CAGTAAATCC CTCCAGTGTG GTTAGCGAAA GGATTAGCAG TGTGTGA	1377

25 (231) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) .TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

5	Met Val Asn Leu Arg Asn Ala Val His Ser Phe Leu Val His Leu Ile	1 5 10 15
	Gly Leu Leu Val Trp Gln Cys Asp Ile Ser Val Ser Pro Val Ala Ala	20 25 30
	Ile Val Thr Asp Ile Phe Asn Thr Ser Asp Gly Gly Arg Phe Lys Phe	35 40 45
10	Pro Asp Gly Val Gln Asn Trp Pro Ala Leu Ser Ile Val Ile Ile Ile	50 55 60
	Ile Met Thr Ile Gly Gly Asn Ile Leu Val Ile Met Ala Val Ser Met	65 70 75 80
15	Glu Lys Lys Leu His Asn Ala Thr Asn Tyr Phe Leu Met Ser Leu Ala	85 90 95
	Ile Ala Asp Met Leu Val Gly Leu Leu Val Met Pro Leu Ser Leu Leu	100 105 110
	Ala Ile Leu Tyr Asp Tyr Val Trp Pro Leu Pro Arg Tyr Leu Cys Pro	115 120 125
20	Val Trp Ile Ser Leu Asp Val Leu Phe Ser Thr Ala Ser Ile Met His	130 135 140
	Leu Cys Ala Ile Ser Leu Asp Arg Tyr Val Ala Ile Arg Asn Pro Ile	145 150 155 160
25	Glu His Ser Arg Phe Asn Ser Arg Thr Lys Ala Ile Met Lys Ile Ala	165 170 175
	Ile Val Trp Ala Ile Ser Ile Gly Val Ser Val Pro Ile Pro Val Ile	180 185 190
	Gly Leu Arg Asp Glu Glu Lys Val Phe Val Asn Asn Thr Thr Cys Val	195 200 205
30	Leu Asn Asp Pro Asn Phe Val Leu Ile Gly Ser Phe Val Ala Phe Phe	210 215 220
	Ile Pro Leu Thr Ile Met Val Ile Thr Tyr Cys Leu Thr Ile Tyr Val	225 230 235 240
35	Leu Arg Arg Gln Ala Leu Met Leu Leu His Gly His Thr Glu Glu Pro	245 250 255
	Pro Gly Leu Ser Leu Asp Phe Leu Lys Cys Cys Lys Arg Asn Thr Ala	

198

	260	265	270
	Glu Glu Glu Asn Ser Ala Asn Pro Asn Gln Asp Gln Asn Ala Arg Arg		
	275	280	285
5	Arg Lys Lys Lys Glu Arg Arg Pro Arg Gly Thr Met Gln Ala Ile Asn		
	290	295	300
	Asn Glu Arg Lys Ala Lys Lys Val Leu Gly Ile Val Phe Phe Val Phe		
	305	310	315 320
	Leu Ile Met Trp Cys Pro Phe Phe Ile Thr Asn Ile Leu Ser Val Leu		
	325	330	335
10	Cys Glu Lys Ser Cys Asn Gln Lys Leu Met Glu Lys Leu Leu Asn Val		
	340	345	350
	Phe Val Trp Ile Gly Tyr Val Cys Ser Gly Ile Asn Pro Leu Val Tyr		
	355	360	365
15	Thr Leu Phe Asn Lys Ile Tyr Arg Arg Ala Phe Ser Asn Tyr Leu Arg		
	370	375	380
	Cys Asn Tyr Lys Val Glu Lys Lys Pro Pro Val Arg Gln Ile Pro Arg		
	385	390	395 400
	Val Ala Ala Thr Ala Leu Ser Gly Arg Glu Leu Asn Val Asn Ile Tyr		
	405	410	415
20	Arg His Thr Asn Glu Pro Val Ile Glu Lys Ala Ser Asp Asn Glu Pro		
	420	425	430
	Gly Ile Glu Met Gln Val Glu Asn Leu Glu Leu Pro Val Asn Pro Ser		
	435	440	445
25	Ser Val Val Ser Glu Arg Ile Ser Ser Val		
	450	455	

(232) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1068 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

	ATGGATCAGT TCCCTGAATC AGTGACAGAA AACTTTGAGT ACGATGATTT GGCTGAGGCC	60
35	TGTTATATTG GGGACATCGT GGTCTTTGGG ACTGTGTTCC TGTCCATATT CTACTCCGTC	120
	ATCTTTGCCA TTGGCCTGGT GGGAAATTTG TTGTTAGTGT TTGCCCTCAC CAACAGCAAG	180

AAGCCCAAGA GTGTCACCGA CATTACCTC CTGAACCTGG CCTTGTCTGA TCTGCTGTTT 240
 GTAGCCACTT TGCCCTTCTG GACTCACTAT TTGATAAATG AAAAGGGCCT CCACAATGCC 300
 ATGTGCAAAT TCACTACCGC CTTCTTCTTC ATCGGCTTTT TTGGAAGCAT ATTCTTCATC 360
 ACCGTCATCA GCATTGATAG GTACCTGGCC ATCGTCCTGG CCGCCAACTC CATGAACAAC 420
 5 CGGACCGTGC AGCATGGCGT CACCATCAGC CTAGGCGTCT GGGCAGCAGC CATTTTGGTG 480
 GCAGCACCCC AGTTCATGTT CACAAAGCAG AAAGAAAATG AATGCCTTGG TGACTACCCC 540
 GAGGTCTCC AGGAAATCTG GCCCCGTGCTC CGCAATGTGG AAACAAATTT TCTTGGCTTC 600
 CTACTCCCCC TGCTCATTAT GAGTTATTGC TACTTCAGAA TCATCCAGAC GCTGTTTTCC 660
 TGCAAGAACC ACAAGAAAGC CAAAGCCAAG AACTGATCC TTCTGGTGGT CATCGTGTTT 720
 10 TTCCTCTTCT GGACACCCTA CAACGTTATG ATTTTCCTGG AGACGCTTAA GCTCTATGAC 780
 TTCTTTCCCA GTTGTGACAT GAGGAAGGAT CTGAGGCTGG CCCTCAGTGT GACTGAGACG 840
 GTTGCAATTA GCCATTGTTG CCTGAATCCT CTCATCTATG CATTTGCTGG GGAGAAGTTC 900
 AGAAGATACC TTTACCACCT GTATGGGAAA TGCCTGGCTG TCCTGTGTGG GCGCTCAGTC 960
 CACGTTGATT TCTCCTCATC TGAATCACAA AGGAGCAGGC ATGGAAGTGT TCTGAGCAGC 1020
 15 AATTTTACTT ACCACACGAG TGATGGAGAT GCATTGCTCC TTCTCTGA 1068

(233) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 355 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

25 Met Asp Gln Phe Pro Glu Ser Val Thr Glu Asn Phe Glu Tyr Asp Asp
 1 5 10 15
 Leu Ala Glu Ala Cys Tyr Ile Gly Asp Ile Val Val Phe Gly Thr Val
 20 25 30
 Phe Leu Ser Ile Phe Tyr Ser Val Ile Phe Ala Ile Gly Leu Val Gly
 35 40 45
 30 Asn Leu Leu Val Val Phe Ala Leu Thr Asn Ser Lys Lys Pro Lys Ser
 50 55 60
 Val Thr Asp Ile Tyr Leu Leu Asn Leu Ala Leu Ser Asp Leu Leu Phe

200

	65	70	75	80
	Val	Ala Thr	Leu Pro Phe Trp Thr His Tyr	Leu Ile Asn Glu Lys Gly
		85	90	95
5	Leu His Asn Ala Met Cys Lys Phe Thr Thr Ala Phe Phe Phe Ile Gly	100	105	110
	Phe Phe Gly Ser Ile Phe Phe Ile Thr Val Ile Ser Ile Asp Arg Tyr	115	120	125
	Leu Ala Ile Val Leu Ala Ala Asn Ser Met Asn Asn Arg Thr Val Gln	130	135	140
10	His Gly Val Thr Ile Ser Leu Gly Val Trp Ala Ala Ala Ile Leu Val	145	150	155
	Ala Ala Pro Gln Phe Met Phe Thr Lys Gln Lys Glu Asn Glu Cys Leu	165	170	175
15	Gly Asp Tyr Pro Glu Val Leu Gln Glu Ile Trp Pro Val Leu Arg Asn	180	185	190
	Val Glu Thr Asn Phe Leu Gly Phe Leu Leu Pro Leu Leu Ile Met Ser	195	200	205
	Tyr Cys Tyr Phe Arg Ile Ile Gln Thr Leu Phe Ser Cys Lys Asn His	210	215	220
20	Lys Lys Ala Lys Ala Lys Lys Leu Ile Leu Leu Val Val Ile Val Phe	225	230	235
	Phe Leu Phe Trp Thr Pro Tyr Asn Val Met Ile Phe Leu Glu Thr Leu	245	250	255
25	Lys Leu Tyr Asp Phe Phe Pro Ser Cys Asp Met Arg Lys Asp Leu Arg	260	265	270
	Leu Ala Leu Ser Val Thr Glu Thr Val Ala Phe Ser His Cys Cys Leu	275	280	285
	Asn Pro Leu Ile Tyr Ala Phe Ala Gly Glu Lys Phe Arg Arg Tyr Leu	290	295	300
30	Tyr His Leu Tyr Gly Lys Cys Leu Ala Val Leu Cys Gly Arg Ser Val	305	310	315
	His Val Asp Phe Ser Ser Ser Glu Ser Gln Arg Ser Arg His Gly Ser	325	330	335
35	Val Leu Ser Ser Asn Phe Thr Tyr His Thr Ser Asp Gly Asp Ala Leu	340	345	350
	Leu Leu Leu	355		

201

(234) INFORMATION FOR SEQ ID NO:233:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

10 GGCTTAAGAG CATCATCGTG GTGCTGGTG

29

(235) INFORMATION FOR SEQ ID NO:234:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iv) ANTI-SENSE: YES
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

20 GTCACCACCA GCACCACGAT GATGCTCTTA AGCC

34

(236) INFORMATION FOR SEQ ID NO:235:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

CAAAGAAAGT ACTGGGCATC GTCTTCTTCC T

31

30 (237) INFORMATION FOR SEQ ID NO:236:

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

TGCTCTAGAT TCCAGATAGG TGAAACTTG

30

(238) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

10 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

CTAGGGGCAC CATGCAGGCT ATCAACAATG AAAGAAAAGC TAAGAAAGTC

50

(239) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

CAAGGACTTT CTTAGCTTTT CTTTCATTGT TGATAGCCTG CATGGTGCCC

50

(240) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

CGGCGGCAGA AGGCGAAACG CATGATCCTC GCGGT

35

(241) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid

203

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

5 ACCGCGAGGA TCATGCGTTT CGCCTTCTGC CGCCG

35

(242) INFORMATION FOR SEQ ID NO:241:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

10

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

GAGACATATT ATCTGCCACG GAGG

24

15 (243) INFORMATION FOR SEQ ID NO:242:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

20

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

TTGGCATAGA AACCGGACCC AAGG

24

(244) INFORMATION FOR SEQ ID NO:243:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

25

- (ii) MOLECULE TYPE: DNA (genomic)

30

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

TAAGAATTCC ATAAAAATTA TGGAATGG

28

(245) INFORMATION FOR SEQ ID NO:244:

- (i) SEQUENCE CHARACTERISTICS:

204

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

CCAGGATCCA GCTGAAGTCT TCCATCATTC

30

(246) INFORMATION FOR SEQ ID NO:245:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1071 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: DNA (genomic)

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

ATGAATGGGG TCTCGGAGGG GACCAGAGGC TGCAGTGACA GGCAACCTGG GGTCTGACA 60

CGTGATCGCT CTTGTTCCAG GAAGATGAAC TCTTCCGGAT GCCTGTCTGA GGAGGTGGGG 120

TCCCTCCGCC CACTGACTGT GGTATCCTG TCTGCGTCCA TTGTCGTCGG AGTGCTGGGC 180

AATGGGCTGG TGCTGTGGAT GACTGTCTTC CGTATGGCAC GCACGGTCTC CACCGTCTGC 240

20 TTCTTCCACC TGGCCCTTGC CGATTTCATG CTCTCACTGT CTCTGCCCAT TGCCATGTAC 300

TATATTGTCT CCAGGCAGTG GCTCCTCGGA GAGTGGGCCT GCAAACCTA CATCACCTTT 360

GTGTTCTCA GCTACTTTGC CAGTAACTGC CTCCTTGTCT TCATCTCTGT GGACCGTTGC 420

ATCTCTGTCC TCTACCCCGT CTGGGCCCTG AACCACCGCA CTGTGCAGCG GCGAGCTGG 480

CTGGCCTTTG GGTGTGGCT CCTGGCCGCC GCCTTGTGCT CTGCGCACCT GAAATTCGG 540

25 ACAACCAGAA AATGGAATGG CTGTACGCAC TGCTACTTGG CGTTCAACTC TGACAATGAG 600

ACTGCCCAGA TTTGGATTGA AGGGGTCGTG GAGGGACACA TTATAGGGAC CATTGGCCAC 660

TTCCTGCTGG GCTTCTGGG GCCCTTAGCA ATCATAGGCA CCTGCGCCCA CCTCATCCGG 720

GCCAAGCTCT TGCGGGAGGG CTGGGTCCAT GCCAACCGGC CCGCGAGGCT GCTGCTGGTG 780

CTGGTGAGCG CTTTCTTTAT CTTCTGGTCC CCGTTTAACG TGGTGCTGTT GGTCCATCTG 840

30 TGGCGACGGG TGATGCTCAA GGAAATCTAC CACCCCGGA TGCTGCTCAT CCTCCAGGCT 900

AGCTTTGCCT TGGGCTGTGT CAACAGCAGC CTCAACCCCT TCCTCTACGT CTCGTTGGC 960

AGAGATTTCC AAGAAAAGTT TTTCCAGTCT TTGACTTCTG CCCTGGCGAG GGC GTTTGGA 1020
 GAGGAGGAGT TTCTGTCATC CTGTCCCCGT GGCAACGCCC CCCGGGAATG A 1071

(247) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:
 5 (A) LENGTH: 356 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

Met	Asn	Gly	Val	Ser	Glu	Gly	Thr	Arg	Gly	Cys	Ser	Asp	Arg	Gln	Pro	1	5	10	15
Gly	Val	Leu	Thr	Arg	Asp	Arg	Ser	Cys	Ser	Arg	Lys	Met	Asn	Ser	Ser	20	25	30	
Gly	Cys	Leu	Ser	Glu	Glu	Val	Gly	Ser	Leu	Arg	Pro	Leu	Thr	Val	Val	35	40	45	
Ile	Leu	Ser	Ala	Ser	Ile	Val	Val	Gly	Val	Leu	Gly	Asn	Gly	Leu	Val	50	55	60	
Leu	Trp	Met	Thr	Val	Phe	Arg	Met	Ala	Arg	Thr	Val	Ser	Thr	Val	Cys	65	70	75	80
Phe	Phe	His	Leu	Ala	Leu	Ala	Asp	Phe	Met	Leu	Ser	Leu	Ser	Leu	Pro	85	90	95	
Ile	Ala	Met	Tyr	Tyr	Ile	Val	Ser	Arg	Gln	Trp	Leu	Leu	Gly	Glu	Trp	100	105	110	
Ala	Cys	Lys	Leu	Tyr	Ile	Thr	Phe	Val	Phe	Leu	Ser	Tyr	Phe	Ala	Ser	115	120	125	
Asn	Cys	Leu	Leu	Val	Phe	Ile	Ser	Val	Asp	Arg	Cys	Ile	Ser	Val	Leu	130	135	140	
Tyr	Pro	Val	Trp	Ala	Leu	Asn	His	Arg	Thr	Val	Gln	Arg	Ala	Ser	Trp	145	150	155	160
Leu	Ala	Phe	Gly	Val	Trp	Leu	Leu	Ala	Ala	Ala	Leu	Cys	Ser	Ala	His	165	170	175	
Leu	Lys	Phe	Arg	Thr	Thr	Arg	Lys	Trp	Asn	Gly	Cys	Thr	His	Cys	Tyr	180	185	190	
Leu	Ala	Phe	Asn	Ser	Asp	Asn	Glu	Thr	Ala	Gln	Ile	Trp	Ile	Glu	Gly	195	200	205	

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Val Val Glu Gly His Ile Ile Gly Thr Ile Gly His Phe Leu Leu Gly
 210 215 220

Phe Leu Gly Pro Leu Ala Ile Ile Gly Thr Cys Ala His Leu Ile Arg
 225 230 235 240

5 Ala Lys Leu Leu Arg Glu Gly Trp Val His Ala Asn Arg Pro Ala Arg
 245 250 255

Leu Leu Leu Val Leu Val Ser Ala Phe Phe Ile Phe Trp Ser Pro Phe
 260 265 270

10 Asn Val Val Leu Leu Val His Leu Trp Arg Arg Val Met Leu Lys Glu
 275 280 285

Ile Tyr His Pro Arg Met Leu Leu Ile Leu Gln Ala Ser Phe Ala Leu
 290 295 300

Gly Cys Val Asn Ser Ser Leu Asn Pro Phe Leu Tyr Val Phe Val Gly
 305 310 315 320

15 Arg Asp Phe Gln Glu Lys Phe Phe Gln Ser Leu Thr Ser Ala Leu Ala
 325 330 335

Arg Ala Phe Gly Glu Glu Glu Phe Leu Ser Ser Cys Pro Arg Gly Asn
 340 345 350

20 Ala Pro Arg Glu
 355

(248) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

GCAGAATTCG GCGGCCCAT GGACCTGCCC CC

32

30 (249) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

GCTGGATCCC CCGAGCAGTG GCGTTACTTC

30

(250) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 903 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

10 ATGGACCTGC CCCCAGCT CTCCTCGGC CTCTATGTGG CCGCCTTTC GCTGGGCTTC 60
CCGCTCAACG TCCTGGCCAT CCGAGGCGCG ACGGCCACG CCCGGCTCCG TCTACCCCT 120
AGCCTGGTCT ACGCCCTGAA CCTGGGCTGC TCCGACCTGC TGCTGACAGT CTCTCTGCCC 180
CTGAAGGCGG TGGAGGCGCT AGCCTCCGGG GCCTGGCCTC TGCCGGCCTC GCTGTGCCCC 240
GTCTTCGCGG TGGCCCACTT CTCCCACTC TATGCCGGCG GGGGCTTCCT GGCCGCCCTG 300
15 AGTGCAGGCC GCTACCTGGG AGCAGCCTTC CCCTTGGGCT ACCAAGCCTT CCGGAGGCCG 360
TGCTATTCTT GGGGGGTGTG CGCGGCCATC TGGGCCCTCG TCCTGTGTCA CCTGGGTCTG 420
GTCTTTGGGT TGGAGGCTCC AGGAGGCTGG CTGGACCACA GCAACACCTC CCTGGGCATC 480
AACACACCGG TCAACGGCTC TCCGGTCTGC CTGGAGGCCT GGGACCCGGC CTCTGCCGGC 540
CCGGCCCGCT TCAGCCTCTC TCTCCTGCTC TTTTCTCTGC CCTTGGCCAT CACAGCCTTC 600
20 TGCTACGTGG GCTGCCTCCG GGCCTGGCC CGCTCCGGCC TGACGCACAG GCGGAAGCTG 660
CGGGCCGCCT GGGTGGCCGG CGGGGCCCTC CTCACGCTGC TGCTCTGCGT AGGACCCTAC 720
AACGCCTCCA ACGTGGCCAG CTTCCTGTAC CCAATCTAG GAGGCTCCTG GCGGAAGCTG 780
GGGCTCATCA CGGGTGCCTG GAGTGTGGTG CTTAATCCGC TGGTGACCGG TTACTTGGA 840
AGGGGTCTG GCCTGAAGAC AGTGTGTGCG GCAAGAACGC AAGGGGGCAA GTCCAGAAG 900
25 TAA 903

(251) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 300 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

	Met	Asp	Leu	Pro	Pro	Gln	Leu	Ser	Phe	Gly	Leu	Tyr	Val	Ala	Ala	Phe	
	1				5					10					15		
5	Ala	Leu	Gly	Phe	Pro	Leu	Asn	Val	Leu	Ala	Ile	Arg	Gly	Ala	Thr	Ala	
			20						25					30			
	His	Ala	Arg	Leu	Arg	Leu	Thr	Pro	Ser	Leu	Val	Tyr	Ala	Leu	Asn	Leu	
		35					40					45					
10	Gly	Cys	Ser	Asp	Leu	Leu	Leu	Thr	Val	Ser	Leu	Pro	Leu	Lys	Ala	Val	
		50				55					60						
	Glu	Ala	Leu	Ala	Ser	Gly	Ala	Trp	Pro	Leu	Pro	Ala	Ser	Leu	Cys	Pro	
	65					70				75					80		
	Val	Phe	Ala	Val	Ala	His	Phe	Phe	Pro	Leu	Tyr	Ala	Gly	Gly	Gly	Phe	
				85					90					95			
15	Leu	Ala	Ala	Leu	Ser	Ala	Gly	Arg	Tyr	Leu	Gly	Ala	Ala	Phe	Pro	Leu	
				100					105					110			
	Gly	Tyr	Gln	Ala	Phe	Arg	Arg	Pro	Cys	Tyr	Ser	Trp	Gly	Val	Cys	Ala	
		115					120						125				
20	Ala	Ile	Trp	Ala	Leu	Val	Leu	Cys	His	Leu	Gly	Leu	Val	Phe	Gly	Leu	
		130				135						140					
	Glu	Ala	Pro	Gly	Gly	Trp	Leu	Asp	His	Ser	Asn	Thr	Ser	Leu	Gly	Ile	
	145					150					155				160		
	Asn	Thr	Pro	Val	Asn	Gly	Ser	Pro	Val	Cys	Leu	Glu	Ala	Trp	Asp	Pro	
				165						170					175		
25	Ala	Ser	Ala	Gly	Pro	Ala	Arg	Phe	Ser	Leu	Ser	Leu	Leu	Leu	Phe	Phe	
				180					185					190			
	Leu	Pro	Leu	Ala	Ile	Thr	Ala	Phe	Cys	Tyr	Val	Gly	Cys	Leu	Arg	Ala	
		195					200						205				
30	Leu	Ala	Arg	Ser	Gly	Leu	Thr	His	Arg	Arg	Lys	Leu	Arg	Ala	Ala	Trp	
		210					215						220				
	Val	Ala	Gly	Gly	Ala	Leu	Leu	Thr	Leu	Leu	Leu	Cys	Val	Gly	Pro	Tyr	
	225					230					235				240		
	Asn	Ala	Ser	Asn	Val	Ala	Ser	Phe	Leu	Tyr	Pro	Asn	Leu	Gly	Gly	Ser	
				245						250				255			
35	Trp	Arg	Lys	Leu	Gly	Leu	Ile	Thr	Gly	Ala	Trp	Ser	Val	Val	Leu	Asn	
			260				265							270			
	Pro	Leu	Val	Thr	Gly	Tyr	Leu	Gly	Arg	Gly	Pro	Gly	Leu	Lys	Thr	Val	

209

275

280

285

Cys Ala Ala Arg Thr Gln Gly Gly Lys Ser Gln Lys
 290 295 300

(252) INFORMATION FOR SEQ ID NO:251:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 10 (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

CTCAAGCTTA CTCTCTCTCA CCAGTGGCCA C

31

(253) INFORMATION FOR SEQ ID NO:252:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

CCCTCCTCCC CCGGAGGACC TAGC

24

(254) INFORMATION FOR SEQ ID NO:253:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1041 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

30 ATGGATACAG GCCCCGACCA GTCCTACTTC TCCGGCAATC ACTGGTTCGT CTTCTCGGTG 60
 TACCTTCTCA CTTTCCTGGT GGGGCTCCCC CTCAACCTGC TGGCCCTGGT GGTCTTCGTG 120
 GGCAAGCTGC AGCGCCGCCC GGTGGCCGTG GACGTGCTCC TGCTCAACCT GACCGCCTCG 180
 GACCTGCTCC TGCTGCTGTT CCTGCCTTTC CGCATGGTGG AGGCAGCCAA TGGCATGCAC 240
 TGGCCCCCTGC CCTTCATCCT CTGCCCCACTC TCTGGATTCA TCTTCTTCAC CACCATCTAT 300

210

CTCACCGCCC TCTTCCTGGC AGCTGTGAGC ATTGAACGCT TCCTGAGTGT GGCCACCCA 360
 CTGTGGTACA AGACCCGGCC GAGGCTGGGG CAGGCAGGTC TGGTGAGTGT GGCCTGCTGG 420
 CTGTTGGCCT CTGCTCACTG CAGCGTGGTC TACGTCATAG AATTCTCAGG GGACATCTCC 480
 CACAGCCAGG GCACCAATGG GACCTGCTAC CTGGAGTTCC GGAAGGACCA GCTAGCCATC 540
 5 CTCCTGCCCCG TCGGGCTGGA GATGGCTGTG GTCCTCTTTG TGGTCCCGCT GATCATCACC 600
 AGCTACTGCT ACAGCCGCCT GGTGTGGATC CTCGGCAGAG GGGGCAGCCA CCGCCGGCAG 660
 AGGAGGGTGG CGGGGCTGTT GCGGCCACG CTGCTCAACT TCCTTGTCTG CTTTGGGCCC 720
 TACAACGTGT CCCATGTCGT GGGCTATATC TCGGGTGAAG GCCCGGCATG GAGGATCTAC 780
 GTGACGCTTC TCAGCACCTT GAACTCCTGT GTCGACCCCT TTGTCTACTA CTTCTCCTCC 840
 10 TCCGGGTTCC AAGCCGACTT TCATGAGCTG CTGAGGAGGT TGTGTGGGCT CTGGGGCCAG 900
 TGGCAGCAGG AGAGCAGCAT GGAGCTGAAG GAGCAGAAGG GAGGGGAGGA GCAGAGAGCG 960
 GACCGACCAG CTGAAAGAAA GACCAGTGAA CACTCACAGG GCTGTGGAAC TGGTGGCCAG 1020
 GTGGCCTGTG CTGAAAGCTA G 1041

(255) INFORMATION FOR SEQ ID NO:254:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 346 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

- 20 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

Met Asp Thr Gly Pro Asp Gln Ser Tyr Phe Ser Gly Asn His Trp Phe
 1 5 10 15
 Val Phe Ser Val Tyr Leu Leu Thr Phe Leu Val Gly Leu Pro Leu Asn
 20 25 30
 25 Leu Leu Ala Leu Val Val Phe Val Gly Lys Leu Gln Arg Arg Pro Val
 35 40 45
 Ala Val Asp Val Leu Leu Leu Asn Leu Thr Ala Ser Asp Leu Leu Leu
 50 55 60
 30 Leu Leu Phe Leu Pro Phe Arg Met Val Glu Ala Ala Asn Gly Met His
 65 70 75 80
 Trp Pro Leu Pro Phe Ile Leu Cys Pro Leu Ser Gly Phe Ile Phe Phe
 85 90 95

211

	Thr	Thr	Ile	Tyr	Leu	Thr	Ala	Leu	Phe	Leu	Ala	Ala	Val	Ser	Ile	Glu
				100					105					110		
	Arg	Phe	Leu	Ser	Val	Ala	His	Pro	Leu	Trp	Tyr	Lys	Thr	Arg	Pro	Arg
			115					120					125			
5	Leu	Gly	Gln	Ala	Gly	Leu	Val	Ser	Val	Ala	Cys	Trp	Leu	Leu	Ala	Ser
		130					135					140				
	Ala	His	Cys	Ser	Val	Val	Tyr	Val	Ile	Glu	Phe	Ser	Gly	Asp	Ile	Ser
	145					150					155					160
10	His	Ser	Gln	Gly	Thr	Asn	Gly	Thr	Cys	Tyr	Leu	Glu	Phe	Arg	Lys	Asp
				165						170					175	
	Gln	Leu	Ala	Ile	Leu	Leu	Pro	Val	Arg	Leu	Glu	Met	Ala	Val	Val	Leu
				180					185					190		
	Phe	Val	Val	Pro	Leu	Ile	Ile	Thr	Ser	Tyr	Cys	Tyr	Ser	Arg	Leu	Val
		195						200					205			
15	Trp	Ile	Leu	Gly	Arg	Gly	Gly	Ser	His	Arg	Arg	Gln	Arg	Arg	Val	Ala
		210					215					220				
	Gly	Leu	Leu	Ala	Ala	Thr	Leu	Leu	Asn	Phe	Leu	Val	Cys	Phe	Gly	Pro
	225					230					235					240
20	Tyr	Asn	Val	Ser	His	Val	Val	Gly	Tyr	Ile	Cys	Gly	Glu	Ser	Pro	Ala
					245					250					255	
	Trp	Arg	Ile	Tyr	Val	Thr	Leu	Leu	Ser	Thr	Leu	Asn	Ser	Cys	Val	Asp
				260					265					270		
	Pro	Phe	Val	Tyr	Tyr	Phe	Ser	Ser	Ser	Gly	Phe	Gln	Ala	Asp	Phe	His
			275					280					285			
25	Glu	Leu	Leu	Arg	Arg	Leu	Cys	Gly	Leu	Trp	Gly	Gln	Trp	Gln	Gln	Glu
		290					295					300				
	Ser	Ser	Met	Glu	Leu	Lys	Glu	Gln	Lys	Gly	Gly	Glu	Glu	Gln	Arg	Ala
	305					310					315					320
30	Asp	Arg	Pro	Ala	Glu	Arg	Lys	Thr	Ser	Glu	His	Ser	Gln	Gly	Cys	Gly
					325					330					335	
	Thr	Gly	Gly	Gln	Val	Ala	Cys	Ala	Glu	Ser						
				340					345							

(256) INFORMATION FOR SEQ ID NO:255:

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

TTTAAGCTTC CCCTCCAGGA TGCTGCCGGA C

31

(257) INFORMATION FOR SEQ ID NO:256:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: not relevant

10 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

GGCGAATTCT GAAGGTCCAG GGAACTGCT A

31

(258) INFORMATION FOR SEQ ID NO:257:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 993 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

ATGCTGCCGG ACTGGAAGAG CTCCTTGATC CTCATGGCTT ACATCATCAT CTCCTCACT 60
GGCCTCCCTG CCAACCTCCT GGCCCTGCGG GCCTTTGTGG GCGGATCCG CCAGCCCCAG 120
CCTGCACCTG TGCACATCCT CCTGCTGAGC CTGACGCTGG CCGACCTCCT CCTGCTGCTG 180
CTGCTGCCCT TCAAGATCAT CGAGGCTGCG TCGAACTTCC GCTGGTACCT GCCCAAGGTC 240
25 GTCTGCGCCC TCACGAGTTT TGGCTTCTAC AGCAGCATCT ACTGCAGCAC GTGGCTCCTG 300
GCGGGCATCA GCATCGAGCG CTACCTGGGA GTGGCTTTCC CCGTGCAGTA CAAGCTCTCC 360
CGCCGGCCTC TGTATGGAGT GATTGCAGCT CTGGTGGCCT GGGTTATGTC CTTTGGTCAC 420
TGCACCATCG TGATCATCGT TCAATACTTG AACACGACTG AGCAGGTCAG AAGTGGCAAT 480
GAAATTACCT GCTACGAGAA CTTACCGAT AACCAGTTGG ACGTGGTGCT GCCCGTCCGG 540
30 CTGGAGCTGT GCCTGGTGCT CTTCTTCATC CCCATGGCAG TCACCATCTT CTGCTACTGG 600
CGTTTTGTGT GGATCATGCT CTCCCAGCCC CTTGTGGGGG CCCAGAGGCG GCGCCGAGCC 660
GTGGGGCTGG CTGTGGTGAC GCTGCTCAAT TTCCTGGTGT GCTTCGGACC TTACAACGTG 720

213

TCCCACCTGG TGGGGTATCA CCAGAGAAAA AGCCCCTGGT GGCGGTCAAT AGCCGTGGTG 780
 TTCAGTTCAC TCAACGCCAG TCTGGACCCC CTGCTCTTCT ATTTCTCTTC TTCAGTGGTG 840
 CGCAGGGCAT TTGGGAGAGG GCTGCAGGTG CTGCGGAATC AGGGCTCCTC CCTGTTGGGA 900
 CGCAGAGGCA AAGACACAGC AGAGGGGACA AATGAGGACA GGGGTGTGGG TCAAGGAGAA 960
 5 GGGATGCCAA GTTCGGACTT CACTACAGAG TAG 993

(259) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 362 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

15 Met Leu Pro Asp Trp Lys Ser Ser Leu Ile Leu Met Ala Tyr Ile Ile
 1 5 10 15
 Ile Phe Leu Thr Gly Leu Pro Ala Asn Leu Leu Ala Leu Arg Ala Phe
 20 25 30
 Val Gly Arg Ile Arg Gln Pro Gln Pro Ala Pro Val His Ile Leu Leu
 35 40 45
 20 Leu Ser Leu Thr Leu Ala Asp Leu Leu Leu Leu Leu Leu Pro Phe
 50 55 60
 Lys Ile Ile Glu Ala Ala Ser Asn Phe Arg Trp Tyr Leu Pro Lys Val
 65 70 75 80
 25 Val Cys Ala Leu Thr Ser Phe Gly Phe Tyr Ser Ser Ile Tyr Cys Ser
 85 90 95
 Thr Trp Leu Leu Ala Gly Ile Ser Ile Glu Arg Tyr Leu Gly Val Ala
 100 105 110
 Phe Pro Val Gln Tyr Lys Leu Ser Arg Arg Pro Leu Tyr Gly Val Ile
 115 120 125
 30 Ala Ala Leu Val Ala Trp Val Met Ser Phe Gly His Cys Thr Ile Val
 130 135 140
 Ile Ile Val Gln Tyr Leu Asn Thr Thr Glu Gln Val Arg Ser Gly Asn
 145 150 155 160
 35 Glu Ile Thr Cys Tyr Glu Asn Phe Thr Asp Asn Gln Leu Asp Val Val
 165 170 175

214

Leu Pro Val Arg Leu Glu Leu Cys Leu Val Leu Phe Phe Ile Pro Met
 180 185 190
 Ala Val Thr Ile Phe Cys Tyr Trp Arg Phe Val Trp Ile Met Leu Ser
 195 200 205
 5 Gln Pro Leu Val Gly Ala Gln Arg Arg Arg Arg Ala Val Gly Leu Ala
 210 215 220
 Val Val Thr Leu Leu Asn Phe Leu Val Cys Phe Gly Pro Tyr Asn Val
 225 230 235 240
 10 Ser His Leu Val Gly Tyr His Gln Arg Lys Ser Pro Trp Trp Arg Ser
 245 250 255
 Ile Ala Val Val Phe Ser Ser Leu Asn Ala Ser Leu Asp Pro Leu Leu
 260 265 270
 Phe Tyr Phe Ser Ser Ser Val Val Arg Arg Ala Phe Gly Arg Gly Leu
 275 280 285
 15 Gln Val Leu Arg Asn Gln Gly Ser Ser Leu Leu Gly Arg Arg Gly Lys
 290 295 300
 Asp Thr Ala Glu Gly Thr Asn Glu Asp Arg Gly Val Gly Gln Gly Glu
 305 310 315 320
 20 Gly Met Pro Ser Ser Asp Phe Thr Thr Glu
 325 330

(260) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

CCCAAGCTTC GGGCACCATG GACACCTCCC

30

30 (261) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 35 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

ACAGGATCCA AATGCACAGC ACTGGTAAGC 30

(262) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

10 CTATAACTGG GTTACATGGT TTAAC 25

(263) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

TTTGAATTCA CATATTAATT AGAGACATGG 30

20 (264) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2724 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

ATGGACACCT CCCGGCTCGG TGTGCTCCTG TCCTTGCTGCA GCTGGCGACC 60

GGGGGCAGCT CTCCCAGGTC TGGTGTGTTG CTGAGGGGCT GCCCCACACA CTGTCATTGC 120

30 GAGCCCGACG GCAGGATGTT GCTCAGGGTG GACTGCTCCG ACCTGGGGCT CTCGGAGCTG 180

CCTTCCAACC TCAGCGTCTT CACCTCCTAC CTAGACCTCA GTATGAACAA CATCAGTCAG 240

CTGCTCCCGA ATCCCCTGCC CAGTCTCCGC TTCCTGGAGG AGTTACGTCT TCGGGGAAAC 300

GCTCTGACAT ACATTCCCAA GGGAGCATTC ACTGGCCTTT ACAGTCTTAA AGTTCTTATG 360

	CTGCAGAATA ATCAGCTAAG ACACGTACCC ACAGAAGCTC TGCAGAATTT GCGAAGCCTT	420
	CAATCCCTGC GTCTGGATGC TAACCACATC AGCTATGTGC CCCCAGCTG TTTCAGTGGC	480
	CTGCATTCCC TGAGGCACCT GTGGCTGGAT GACAATGCGT TAACAGAAAT CCCCCTCCAG	540
	GCTTTTAGAA GTTTATCGGC ATTGCAAGCC ATGACCTTGG CCCTGAACAA AATACACCAC	600
5	ATACCAGACT ATGCCTTTGG AAACCTCTCC AGCTTGGTAG TTCTACATCT CCATAACAAT	660
	AGAATCCACT CCCTGGGAAA GAAATGCTTT GATGGGCTCC ACAGCCTAGA GACTTTAGAT	720
	TTAAATTACA ATAACCTTGA TGAATCCCC ACTGCAATTA GGACACTCTC CAACCTTAAA	780
	GAACTAGGAT TTCATAGCAA CAATATCAGG TCGATACCTG AGAAAGCATT TGTAGGCAAC	840
	CCTTCTCTTA TTACAATACA TTTCTATGAC AATCCCATCC AATTTGTTGG GAGATCTGCT	900
10	TTTCAACATT TACCTGAACT AAGAACACTG ACTCTGAATG GTGCCTCACA AATAACTGAA	960
	TTTCTGATT TAACTGGAAC TGCAAACCTG GAGAGTCTGA CTTTAACTGG AGCACAGATC	1020
	TCATCTCTTC CTCAAACCGT CTGCAATCAG TTACCTAATC TCCAAGTGCT AGATCTGTCT	1080
	TACAACTAT TAGAAGATTT ACCCAGTTTT TCAGTCTGCC AAAAGCTTCA GAAAATTGAC	1140
	CTAAGACATA ATGAAATCTA CGAAATTAAA GTTGACACTT TCCAGCAGTT GCTTAGCCTC	1200
15	CGATCGCTGA ATTTGGCTTG GAACAAAATT GCTATTATTC ACCCCAATGC ATTTTCCACT	1260
	TTGCCATCCC TAATAAGCT GGACCTATCG TCCAACCTCC TGTCGTCTTT TCCTATAACT	1320
	GGGTTACATG GTTTAACTCA CTTAAAATTA ACAGGAAATC ATGCCTTACA GAGCTTGATA	1380
	TCATCTGAAA ACTTTCCAGA ACTCAAGGTT ATAGAAATGC CTTATGCTTA CCAGTGCTGT	1440
	GCATTTGGAG TGTGTGAGAA TGCCTATAAG ATTTCTAATC AATGGAATAA AGGTGACAAC	1500
20	AGCAGTATGG ACGACCTTCA TAAGAAAGAT GCTGGAATGT TTCAGGCTCA AGATGAACGT	1560
	GACCTTGAAG ATTTCTGCT TGACTTTGAG GAAGACCTGA AAGCCCTTCA TTCAGTGCAG	1620
	TGTTACCTT CCCCAGGCCC CTTCAAACCC TGTGAACACC TGCTTGATGG CTGGCTGATC	1680
	AGAATTGGAG TGTGGACCAT AGCAGTTCTG GCACTTACTT GTAATGCTTT GGTGACTTCA	1740
	ACAGTTTTC AATCCCCTCT GTACATTTCC CCCATTAAAC TGTTAATTGG GGTGATCGCA	1800
25	GCACTGAACA TGCTCACGGG AGTCTCCAGT GCCGTGCTGG CTGGTGTGGA TGCGTTCACT	1860
	TTTGGCAGCT TTGCACGACA TGGTGCCTGG TGGGAGAATG GGGTTGGTTG CCATGTCATT	1920
	GGTTTTTGT CCATTTTGC TTCAGAATCA TCTGTTTTCC TGCTTACTCT GGCAGCCCTG	1980
	GAGCGTGGGT TCTCTGTGAA ATATTCTGCA AAATTTGAAA CGAAAGCTCC ATTTTCTAGC	2040

217

CTGAAAGTAA TCATTTTGCT CTGTGCCCTG CTGGCCTTGA CCATGGCCGC AGTTCCTCTG 2100
 CTGGGTGGCA GCAAGTATGG CGCCTCCCCT CTCTGCCTGC CTTTGCCTTT TGGGGAGCCC 2160
 AGCACCATGG GCTACATGGT CGCTCTCATC TTGCTCAATT CCCTTTGCTT CCTCATGATG 2220
 ACCATTGCCT ACACCAAGCT CTACTGCAAT TTGGACAAGG GAGACCTGGA GAATATTTGG 2280
 5 GACTGCTCTA TGGTAAAACA CATTGCCCTG TTGCTCTTCA CCAACTGCAT CCTAAACTGC 2340
 CCTGTGGCTT TCTTGTCTT CTCCTCTTTA ATAAACCTTA CATTTATCAG TCCTGAAGTA 2400
 ATTAAGTTTA TCCTTCTGGT GGTAGTCCCA CTTCTGCAT GTCTCAATCC CCTTCTCTAC 2460
 ATCTTGTTCA ATCCTCACTT TAAGGAGGAT CTGGTGAGCC TGAGAAAGCA AACCTACGTC 2520
 TGGACAAGAT CAAAACACCC AAGCTTGATG TCAATTAACCT CTGATGATGT CGAAAAACAG 2580
 10 TCCTGTGACT CAACTCAAGC CTTGGTAACC TTTACCAGCT CCAGCATCAC TTATGACCTG 2640
 CCTCCAGTT CCGTGCCATC ACCAGCTTAT CCAGTGACTG AGAGCTGCCA TCTTTCCTCT 2700
 GTGGCATTG TCCCATGTCT CTAA 2724

(265) INFORMATION FOR SEQ ID NO:264:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 907 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant
 (ii) MOLECULE TYPE: protein

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:
 Met Asp Thr Ser Arg Leu Gly Val Leu Leu Ser Leu Pro Val Leu Leu
 1 5 10 15
 Gln Leu Ala Thr Gly Gly Ser Ser Pro Arg Ser Gly Val Leu Leu Arg
 20 25 30
 25 Gly Cys Pro Thr His Cys His Cys Glu Pro Asp Gly Arg Met Leu Leu
 35 40 45
 Arg Val Asp Cys Ser Asp Leu Gly Leu Ser Glu Leu Pro Ser Asn Leu
 50 55 60
 30 Ser Val Phe Thr Ser Tyr Leu Asp Leu Ser Met Asn Asn Ile Ser Gln
 65 70 75 80
 Leu Leu Pro Asn Pro Leu Pro Ser Leu Arg Phe Leu Glu Glu Leu Arg
 85 90 95
 Leu Ala Gly Asn Ala Leu Thr Tyr Ile Pro Lys Gly Ala Phe Thr Gly

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	100	105	110
	Leu Tyr Ser Leu Lys Val Leu Met Leu Gln Asn Asn Gln Leu Arg His		
	115	120	125
5	Val Pro Thr Glu Ala Leu Gln Asn Leu Arg Ser Leu Gln Ser Leu Arg		
	130	135	140
	Leu Asp Ala Asn His Ile Ser Tyr Val Pro Pro Ser Cys Phe Ser Gly		
	145	150	155
	Leu His Ser Leu Arg His Leu Trp Leu Asp Asp Asn Ala Leu Thr Glu		
	165	170	175
10	Ile Pro Val Gln Ala Phe Arg Ser Leu Ser Ala Leu Gln Ala Met Thr		
	180	185	190
	Leu Ala Leu Asn Lys Ile His His Ile Pro Asp Tyr Ala Phe Gly Asn		
	195	200	205
15	Leu Ser Ser Leu Val Val Leu His Leu His Asn Asn Arg Ile His Ser		
	210	215	220
	Leu Gly Lys Lys Cys Phe Asp Gly Leu His Ser Leu Glu Thr Leu Asp		
	225	230	235
	Leu Asn Tyr Asn Asn Leu Asp Glu Phe Pro Thr Ala Ile Arg Thr Leu		
	245	250	255
20	Ser Asn Leu Lys Glu Leu Gly Phe His Ser Asn Asn Ile Arg Ser Ile		
	260	265	270
	Pro Glu Lys Ala Phe Val Gly Asn Pro Ser Leu Ile Thr Ile His Phe		
	275	280	285
25	Tyr Asp Asn Pro Ile Gln Phe Val Gly Arg Ser Ala Phe Gln His Leu		
	290	295	300
	Pro Glu Leu Arg Thr Leu Thr Leu Asn Gly Ala Ser Gln Ile Thr Glu		
	305	310	315
	Phe Pro Asp Leu Thr Gly Thr Ala Asn Leu Glu Ser Leu Thr Leu Thr		
	325	330	335
30	Gly Ala Gln Ile Ser Ser Leu Pro Gln Thr Val Cys Asn Gln Leu Pro		
	340	345	350
	Asn Leu Gln Val Leu Asp Leu Ser Tyr Asn Leu Leu Glu Asp Leu Pro		
	355	360	365
35	Ser Phe Ser Val Cys Gln Lys Leu Gln Lys Ile Asp Leu Arg His Asn		
	370	375	380
	Glu Ile Tyr Glu Ile Lys Val Asp Thr Phe Gln Gln Leu Leu Ser Leu		
	385	390	395
			400

219

	Arg	Ser	Leu	Asn	Leu	Ala	Trp	Asn	Lys	Ile	Ala	Ile	Ile	His	Pro	Asn	405	410	415
	Ala	Phe	Ser	Thr	Leu	Pro	Ser	Leu	Ile	Lys	Leu	Asp	Leu	Ser	Ser	Asn	420	425	430
5	Leu	Leu	Ser	Ser	Phe	Pro	Ile	Thr	Gly	Leu	His	Gly	Leu	Thr	His	Leu	435	440	445
	Lys	Leu	Thr	Gly	Asn	His	Ala	Leu	Gln	Ser	Leu	Ile	Ser	Ser	Glu	Asn	450	455	460
10	Phe	Pro	Glu	Leu	Lys	Val	Ile	Glu	Met	Pro	Tyr	Ala	Tyr	Gln	Cys	Cys	465	470	475
	Ala	Phe	Gly	Val	Cys	Glu	Asn	Ala	Tyr	Lys	Ile	Ser	Asn	Gln	Trp	Asn	485	490	495
	Lys	Gly	Asp	Asn	Ser	Ser	Met	Asp	Asp	Leu	His	Lys	Lys	Asp	Ala	Gly	500	505	510
15	Met	Phe	Gln	Ala	Gln	Asp	Glu	Arg	Asp	Leu	Glu	Asp	Phe	Leu	Leu	Asp	515	520	525
	Phe	Glu	Glu	Asp	Leu	Lys	Ala	Leu	His	Ser	Val	Gln	Cys	Ser	Pro	Ser	530	535	540
20	Pro	Gly	Pro	Phe	Lys	Pro	Cys	Glu	His	Leu	Leu	Asp	Gly	Trp	Leu	Ile	545	550	555
	Arg	Ile	Gly	Val	Trp	Thr	Ile	Ala	Val	Leu	Ala	Leu	Thr	Cys	Asn	Ala	565	570	575
	Leu	Val	Thr	Ser	Thr	Val	Phe	Arg	Ser	Pro	Leu	Tyr	Ile	Ser	Pro	Ile	580	585	590
25	Lys	Leu	Leu	Ile	Gly	Val	Ile	Ala	Ala	Val	Asn	Met	Leu	Thr	Gly	Val	595	600	605
	Ser	Ser	Ala	Val	Leu	Ala	Gly	Val	Asp	Ala	Phe	Thr	Phe	Gly	Ser	Phe	610	615	620
30	Ala	Arg	His	Gly	Ala	Trp	Trp	Glu	Asn	Gly	Val	Gly	Cys	His	Val	Ile	625	630	635
	Gly	Phe	Leu	Ser	Ile	Phe	Ala	Ser	Glu	Ser	Ser	Val	Phe	Leu	Leu	Thr	645	650	655
	Leu	Ala	Ala	Leu	Glu	Arg	Gly	Phe	Ser	Val	Lys	Tyr	Ser	Ala	Lys	Phe	660	665	670
35	Glu	Thr	Lys	Ala	Pro	Phe	Ser	Ser	Leu	Lys	Val	Ile	Ile	Leu	Leu	Cys	675	680	685
	Ala	Leu	Leu	Ala	Leu	Thr	Met	Ala	Ala	Val	Pro	Leu	Leu	Gly	Gly	Ser			

220

	690	695	700
	Lys Tyr Gly Ala Ser Pro Leu Cys Leu Pro Leu Pro Phe Gly Glu Pro		
	705	710	715 720
5	Ser Thr Met Gly Tyr Met Val Ala Leu Ile Leu Leu Asn Ser Leu Cys		
		725	730 735
	Phe Leu Met Met Thr Ile Ala Tyr Thr Lys Leu Tyr Cys Asn Leu Asp		
		740	745 750
	Lys Gly Asp Leu Glu Asn Ile Trp Asp Cys Ser Met Val Lys His Ile		
		755	760 765
10	Ala Leu Leu Leu Phe Thr Asn Cys Ile Leu Asn Cys Pro Val Ala Phe		
		770	775 780
	Leu Ser Phe Ser Ser Leu Ile Asn Leu Thr Phe Ile Ser Pro Glu Val		
		785	790 795 800
15	Ile Lys Phe Ile Leu Leu Val Val Val Pro Leu Pro Ala Cys Leu Asn		
		805	810 815
	Pro Leu Leu Tyr Ile Leu Phe Asn Pro His Phe Lys Glu Asp Leu Val		
		820	825 830
	Ser Leu Arg Lys Gln Thr Tyr Val Trp Thr Arg Ser Lys His Pro Ser		
		835	840 845
20	Leu Met Ser Ile Asn Ser Asp Asp Val Glu Lys Gln Ser Cys Asp Ser		
		850	855 860
	Thr Gln Ala Leu Val Thr Phe Thr Ser Ser Ser Ile Thr Tyr Asp Leu		
		865	870 875 880
25	Pro Pro Ser Ser Val Pro Ser Pro Ala Tyr Pro Val Thr Glu Ser Cys		
		885	890 895
	His Leu Ser Ser Val Ala Phe Val Pro Cys Leu		
		900	905

(266) INFORMATION FOR SEQ ID NO:265:

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

CGGAAGCTGC GGGCCAAATG GGTGGCCGGC

30

221

(267) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

CAGAGGAGGG TGAAGGGGCT GTTGGCG

27

10 (268) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

GGCGGCGCCG AGCCAAGGGG CTGGCTGTGG

30

(269) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

GGGACTGCTC TATGAAAAAA CACATTGCCC TG

32

(270) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1071 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

ATGAATGGGG TCTCGGAGGG GACCAGAGGC TGCAGTGACA GGCAACCTGG GGTCTGACA

60

222

CGTGATCGCT CTTGTTCCAG GAAGATGAAC TCTTCCGGAT GCCTGTCTGA GGAGGTGGGG 120
 TCCCTCCGCC CACTGACTGT GGTTATCCTG TCTGCGTCCA TTGTCGTCGG AGTGCTGGGE 180
 AATGGGCTGG TGCTGTGGAT GACTGTCTTC CGTATGGCAC GCACGGTCTC CACCGTCTGC 240
 TTCTTCCACC TGGCCCTTGC CGATTTCATG CTCTCACTGT CTCTGCCCAT TGCCATGTAC 300
 5 TATATTGTCT CCAGGCAGTG GCTCCTCGGA GAGTGGGCCT GCAAACCTA CATCACCTTT 360
 GTGTTCTCA GCTACTTTGC CAGTAACTGC CTCCTTGTCT TCATCTCTGT GGACCGTTGC 420
 ATCTCTGTCC TCTACCCCGT CTGGGCCCTG AACCACCGCA CTGTGCAGCG GGCGAGCTGG 480
 CTGGCCTTTG GGGTGTGGCT CCTGGCCGCC GCCTTGTGCT CTGCGCACCT GAAATTCGG 540
 ACAACCAGAA AATGGAATGG CTGTACGCAC TGCTACTTGG CGTTCAACTC TGACAATGAG 600
 10 ACTGCCCAGA TTTGGATTGA AGGGGTCGTG GAGGGACACA TTATAGGGAC CATTGGCCAC 660
 TTCCTGCTGG GCTTCCTGGG GCCCTTAGCA ATCATAGGCA CCTGCGCCCA CCTCATCCGG 720
 GCCAAGCTCT TGCGGGAGGG CTGGGTCCAT GCCAACCGGC CCAAGAGGCT GCTGCTGGTG 780
 CTGGTGAGCG CTTTCTTTAT CTTCTGGTCC CCGTTTAACG TGGTGCTGTT GGTCCATCTG 840
 TGGCGACGGG TGATGCTCAA GGAAATCTAC CACCCCCGGA TGCTGCTCAT CCTCCAGGCT 900
 15 AGCTTTGCCT TGGGCTGTGT CAACAGCAGC CTCAACCCCT TCCTCTACGT CTTGCTTGGC 960
 AGAGATTTCC AAGAAAAGTT TTTCCAGTCT TTGACTTCTG CCCTGGCGAG GGCGTTTGA 1020
 GAGGAGGAGT TTCTGTCATC CTGTCCCCGT GGCAACGCCC CCCGGGAATG A 1071

(271) INFORMATION FOR SEQ ID NO:270:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 356 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant
 (ii) MOLECULE TYPE: protein
 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:
 Met Asn Gly Val Ser Glu Gly Thr Arg Gly Cys Ser Asp Arg Gln Pro
 1 5 10 15
 Gly Val Leu Thr Arg Asp Arg Ser Cys Ser Arg Lys Met Asn Ser Ser
 20 25 30
 30 Gly Cys Leu Ser Glu Glu Val Gly Ser Leu Arg Pro Leu Thr Val Val
 35 40 45

223

Ile Leu Ser Ala Ser Ile Val Val Gly Val Leu Gly Asn Gly Leu Val
 50 55 60

Leu Trp Met Thr Val Phe Arg Met Ala Arg Thr Val Ser Thr Val Cys
 65 70 75 80

5 Phe Phe His Leu Ala Leu Ala Asp Phe Met Leu Ser Leu Ser Leu Pro
 85 90 95

Ile Ala Met Tyr Tyr Ile Val Ser Arg Gln Trp Leu Leu Gly Glu Trp
 100 105 110

10 Ala Cys Lys Leu Tyr Ile Thr Phe Val Phe Leu Ser Tyr Phe Ala Ser
 115 120 125

Asn Cys Leu Leu Val Phe Ile Ser Val Asp Arg Cys Ile Ser Val Leu
 130 135 140

Tyr Pro Val Trp Ala Leu Asn His Arg Thr Val Gln Arg Ala Ser Trp
 145 150 155 160

15 Leu Ala Phe Gly Val Trp Leu Leu Ala Ala Leu Cys Ser Ala His
 165 170 175

Leu Lys Phe Arg Thr Thr Arg Lys Trp Asn Gly Cys Thr His Cys Tyr
 180 185 190

20 Leu Ala Phe Asn Ser Asp Asn Glu Thr Ala Gln Ile Trp Ile Glu Gly
 195 200 205

Val Val Glu Gly His Ile Ile Gly Thr Ile Gly His Phe Leu Leu Gly
 210 215 220

Phe Leu Gly Pro Leu Ala Ile Ile Gly Thr Cys Ala His Leu Ile Arg
 225 230 235 240

25 Ala Lys Leu Leu Arg Glu Gly Trp Val His Ala Asn Arg Pro Lys Arg
 245 250 255

Leu Leu Leu Val Leu Val Ser Ala Phe Phe Ile Phe Trp Ser Pro Phe
 260 265 270

30 Asn Val Val Leu Leu Val His Leu Trp Arg Arg Val Met Leu Lys Glu
 275 280 285

Ile Tyr His Pro Arg Met Leu Leu Ile Leu Gln Ala Ser Phe Ala Leu
 290 295 300

Gly Cys Val Asn Ser Ser Leu Asn Pro Phe Leu Tyr Val Phe Val Gly
 305 310 315 320

35 Arg Asp Phe Gln Glu Lys Phe Phe Gln Ser Leu Thr Ser Ala Leu Ala
 325 330 335

Arg Ala Phe Gly Glu Glu Glu Phe Leu Ser Ser Cys Pro Arg Gly Asn

224

340

345

350

Ala Pro Arg Glu
355

(272) INFORMATION FOR SEQ ID NO:271:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 903 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

ATGGACCTGC CCCCAGCAGCT CTCCTTCGGC CTCTATGTGG CCGCCTTTGC GCTGGGCTTC 60
CCGCTCAACG TCCTGGCCAT CCGAGGCGCG ACGGCCACG CCCGGCTCCG TCTACCCCT 120
15 AGCCTGGTCT ACGCCCTGAA CCTGGGCTGC TCCGACCTGC TGCTGACAGT CTCTCTGCCC 180
CTGAAGGCGG TGGAGGCGCT AGCCTCCGGG GCCTGGCCTC TGCCGGCCTC GCTGTGCCCC 240
GTCTTCGCGG TGGCCCACTT CTTCCCACTC TATGCCGGCG GGGGCTTCCT GGCCGCCCTG 300
AGTGCAGGCC GCTACCTGGG AGCAGCCTTC CCCTTGGGCT ACCAAGCCTT CCGGAGGCCG 360
TGCTATTCCT GGGGGGTGTG CGCGGCCATC TGGGCCCTCG TCCTGTGTCA CCTGGGTCTG 420
20 GTCTTTGGGT TGGAGGCTCC AGGAGGCTGG CTGGACCACA GCAACACCTC CCTGGGCATC 480
AACACACCGG TCAACGGCTC TCCGGTCTGC CTGGAGGCCT GGGACCCGGC CTCTGCCGGC 540
CCGGCCCCGCT TCAGCCTCTC TCTCCTGCTC TTTTCTCTGC CCTTGGCCAT CACAGCCTTC 600
TGCTACGTGG GCTGCCTCCG GGCCTGGCC CGCTCCGGCC TGACGCACAG GCGGAAGCTG 660
CGGGCCAAAT GGGTGGCCGG CGGGGCCCTC CTCACGCTGC TGCTCTGCGT AGGACCCTAC 720
25 AACGCCTCCA ACGTGGCCAG CTTCTGTAC CCAATCTAG GAGGCTCCTG GCGGAAGCTG 780
GGGCTCATCA CGGGTGCCTG GAGTGTGGTG CTTAATCCGC TGGTGACCGG TTACTTGGGA 840
AGGGGTCTTG GCCTGAAGAC AGTGTGTGCG GCAAGAACGC AAGGGGGCAA GTCCCAGAAG 900
TAA 903

(273) INFORMATION FOR SEQ ID NO:272:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 300 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:

225

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

5 Met Asp Leu Pro Pro Gln Leu Ser Phe Gly Leu Tyr Val Ala Ala Phe
 1 5 10 15
 Ala Leu Gly Phe Pro Leu Asn Val Leu Ala Ile Arg Gly Ala Thr Ala
 20 25 30
 His Ala Arg Leu Arg Leu Thr Pro Ser Leu Val Tyr Ala Leu Asn Leu
 35 40 45
 10 Gly Cys Ser Asp Leu Leu Leu Thr Val Ser Leu Pro Leu Lys Ala Val
 50 55 60
 Glu Ala Leu Ala Ser Gly Ala Trp Pro Leu Pro Ala Ser Leu Cys Pro
 65 70 75 80
 15 Val Phe Ala Val Ala His Phe Phe Pro Leu Tyr Ala Gly Gly Gly Phe
 85 90 95
 Leu Ala Ala Leu Ser Ala Gly Arg Tyr Leu Gly Ala Ala Phe Pro Leu
 100 105 110
 Gly Tyr Gln Ala Phe Arg Arg Pro Cys Tyr Ser Trp Gly Val Cys Ala
 115 120 125
 20 Ala Ile Trp Ala Leu Val Leu Cys His Leu Gly Leu Val Phe Gly Leu
 130 135 140
 Glu Ala Pro Gly Gly Trp Leu Asp His Ser Asn Thr Ser Leu Gly Ile
 145 150 155 160
 25 Asn Thr Pro Val Asn Gly Ser Pro Val Cys Leu Glu Ala Trp Asp Pro
 165 170 175
 Ala Ser Ala Gly Pro Ala Arg Phe Ser Leu Ser Leu Leu Leu Phe Phe
 180 185 190
 Leu Pro Leu Ala Ile Thr Ala Phe Cys Tyr Val Gly Cys Leu Arg Ala
 195 200 205
 30 Leu Ala Arg Ser Gly Leu Thr His Arg Arg Lys Leu Arg Ala Lys Trp
 210 215 220
 Val Ala Gly Gly Ala Leu Leu Thr Leu Leu Leu Cys Val Gly Pro Tyr
 225 230 235 240
 35 Asn Ala Ser Asn Val Ala Ser Phe Leu Tyr Pro Asn Leu Gly Gly Ser
 245 250 255
 Trp Arg Lys Leu Gly Leu Ile Thr Gly Ala Trp Ser Val Val Leu Asn

226

260 265 270

Pro Leu Val Thr Gly Tyr Leu Gly Arg Gly Pro Gly Leu Lys Thr Val
 275 280 285

Cys Ala Ala Arg Thr Gln Gly Gly Lys Ser Gln Lys
 290 295 300

5

(274) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1041 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: DNA (genomic)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

ATGGATACAG GCCCCGACCA GTCCTACTTC TCCGGCAATC ACTGGTTCGT CTTCTCGGTG 60

15 TACCTTCTCA CTTTCCTGGT GGGGCTCCCC CTCAACCTGC TGGCCCTGGT GGTCTTCGTG 120

GGCAAGCTGC AGCGCCGCCC GGTGGCCGTG GACGTGCTCC TGCTCAACCT GACCGCCTCG 180

GACCTGCTCC TGCTGCTGTT CCTGCCTTTC CGCATGGTGG AGGCAGCCAA TGGCATGCAC 240

TGGCCCCCTGC CTTTCATCCT CTGCCCCACTC TCTGGATTCA TCTTCTTCAC CACCATCTAT 300

CTCACCGCCC TCTTCCTGGC AGCTGTGAGC ATTGAACGCT TCCTGAGTGT GGCCACCCCA 360

20 CTGTGGTACA AGACCCGGCC GAGGCTGGGG CAGGCAGGTC TGGTGAGTGT GGCCTGCTGG 420

CTGTTGGCCT CTGCTCACTG CAGCGTGGTC TACGTCATAG AATTCTCAGG GGACATCTCC 480

CACAGCCAGG GCACCAATGG GACCTGCTAC CTGGAGTTCC GGAAGGACCA GCTAGCCATC 540

CTCCTGCCCC TGCGGCTGGA GATGGCTGTG GTCCTCTTTG TGGTCCCGCT GATCATCACC 600

AGCTACTGCT ACAGCCGCCT GGTGTGGATC CTCGGCAGAG GGGGCAGCCA CCGCCGGCAG 660

25 AGGAGGGTGA AGGGGCTGTT GGCGGCCACG CTGCTCAACT TCCTTGCTG CTTTGGGCCC 720

TACAACGTGT CCCATGTCGT GGGCTATATC TGCGGTGAAA GCCCGGCATG GAGGATCTAC 780

GTGACGCTTC TCAGCACCCCT GAACTCCTGT GTCGACCCCT TTGTCTACTA CTTCTCCTCC 840

TCCGGGTTCC AAGCCGACTT TCATGAGCTG CTGAGGAGGT TGTGTGGGCT CTGGGGCCAG 900

TGGCAGCAGG AGAGCAGCAT GGAGCTGAAG GAGCAGAAGG GAGGGGAGGA GCAGAGAGCG 960

30 GACCGACCAG CTGAAAGAAA GACCAAGTAA CACTCACAGG GCTGTGGAAC TGGTGGCCAG 1020

GTGGCCTGTG CTGAAAGCTA G 1041

227

(275) INFORMATION FOR SEQ ID NO:274:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 346 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

5 Met Asp Thr Gly Pro Asp Gln Ser Tyr Phe Ser Gly Asn His Trp Phe
 1 5 10 15
 Val Phe Ser Val Tyr Leu Leu Thr Phe Leu Val Gly Leu Pro Leu Asn
 20 25 30
 Leu Leu Ala Leu Val Val Phe Val Gly Lys Leu Gln Arg Arg Pro Val
 35 40 45
 15 Ala Val Asp Val Leu Leu Leu Asn Leu Thr Ala Ser Asp Leu Leu Leu
 50 55 60
 Leu Leu Phe Leu Pro Phe Arg Met Val Glu Ala Ala Asn Gly Met His
 65 70 75 80
 20 Trp Pro Leu Pro Phe Ile Leu Cys Pro Leu Ser Gly Phe Ile Phe Phe
 85 90 95
 Thr Thr Ile Tyr Leu Thr Ala Leu Phe Leu Ala Ala Val Ser Ile Glu
 100 105 110
 Arg Phe Leu Ser Val Ala His Pro Leu Trp Tyr Lys Thr Arg Pro Arg
 115 120 125
 25 Leu Gly Gln Ala Gly Leu Val Ser Val Ala Cys Trp Leu Leu Ala Ser
 130 135 140
 Ala His Cys Ser Val Val Tyr Val Ile Glu Phe Ser Gly Asp Ile Ser
 145 150 155 160
 30 His Ser Gln Gly Thr Asn Gly Thr Cys Tyr Leu Glu Phe Arg Lys Asp
 165 170 175
 Gln Leu Ala Ile Leu Leu Pro Val Arg Leu Glu Met Ala Val Val Leu
 180 185 190
 Phe Val Val Pro Leu Ile Ile Thr Ser Tyr Cys Tyr Ser Arg Leu Val
 195 200 205
 35 Trp Ile Leu Gly Arg Gly Gly Ser His Arg Arg Gln Arg Arg Val Lys
 210 215 220
 Gly Leu Leu Ala Ala Thr Leu Leu Asn Phe Leu Val Cys Phe Gly Pro

228

	225	230	235	240
	Tyr Asn Val Ser His Val Val Gly Tyr Ile Cys Gly Glu Ser Pro Ala	245	250	255
5	Trp Arg Ile Tyr Val Thr Leu Leu Ser Thr Leu Asn Ser Cys Val Asp	260	265	270
	Pro Phe Val Tyr Tyr Phe Ser Ser Ser Gly Phe Gln Ala Asp Phe His	275	280	285
	Glu Leu Leu Arg Arg Leu Cys Gly Leu Trp Gly Gln Trp Gln Gln Glu	290	295	300
10	Ser Ser Met Glu Leu Lys Glu Gln Lys Gly Gly Glu Glu Gln Arg Ala	305	310	315
	Asp Arg Pro Ala Glu Arg Lys Thr Ser Glu His Ser Gln Gly Cys Gly	325	330	335
15	Thr Gly Gly Gln Val Ala Cys Ala Glu Ser	340	345	
	(276) INFORMATION FOR SEQ ID NO:275:			
	(i) SEQUENCE CHARACTERISTICS:			
	(A) LENGTH: 993 base pairs			
20	(B) TYPE: nucleic acid			
	(C) STRANDEDNESS: single			
	(D) TOPOLOGY: linear			
	(ii) MOLECULE TYPE: DNA (genomic)			
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:			
	ATGCTGCCGG ACTGGAAGAG CTCCTTGATC CTCATGGCTT ACATCATCAT CTTCCTCACT			60
25	GGCCTCCCTG CCAACCTCCT GGCCCTGCGG GCCTTTGTGG GCGGGATCCG CCAGCCCCAG			120
	CCTGCACCTG TGCACATCCT CCTGCTGAGC CTGACGCTGG CCGACCTCCT CCTGCTGCTG			180
	CTGCTGCCCT TCAAGATCAT CGAGGCTGCG TCGAACTTCC GCTGGTACCT GCCCAAGGTC			240
	GTCTGCGCCC TCACGAGTTT TGGCTTCTAC AGCAGCATCT ACTGCAGCAC GTGGCTCCTG			300
	GCGGGCATCA GCATCGAGCG CTACCTGGGA GTGGCTTTCC CCGTGAGTA CAAGCTCTCC			360
30	CGCCGGCCTC TGTATGGAGT GATTGCAGCT CTGGTGGCCT GGGTTATGTC CTTTGGTCAC			420
	TGCACCATCG TGATCATCGT TCAATACTTG AACACGACTG AGCAGGTCAG AAGTGGCAAT			480
	GAAATTACCT GCTACGAGAA CTTACCGAT AACCAGTTGG ACGTGGTGCT GCGCGTGGCG			540
	CTGGAGCTGT GCCTGGTGCT CTCTTCATC CCCATGGCAG TCACCATCTT CTGCTACTGG			600

229

CGTTTTGTGT GGATCATGCT CTCCCAGCCC CTTGTGGGGG CCCAGAGGCG GCGCCGAGCC 660
 AAGGGGCTGG CTGTGGTGAC GCTGCTCAAT TTCCTGGTGT GCTTCGGACC TTACAACGTG 720
 TCCCACCTGG TGGGGTATCA CCAGAGAAAA AGCCCCTGGT GCGGGTCAAT AGCCGTGGTG 780
 TTCAGTTCAC TCAACGCCAG TCTGGACCCC CTGCTCTTCT ATTTCTCTTC TTCAGTGGTG 840
 5 CGCAGGGCAT TTGGGAGAGG GCTGCAGGTG CTGCGGAATC AGGGCTCCTC CCTGTTGGGA 900
 CGCAGAGGCA AAGACACAGC AGAGGGGACA AATGAGGACA GGGGTGTGGG TCAAGGAGAA 960
 GGGATGCCAA GTTCGGACTT CACTACAGAG TAG 993

(277) INFORMATION FOR SEQ ID NO:276:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 330 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant
 (ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

Met Leu Pro Asp Trp Lys Ser Ser Leu Ile Leu Met Ala Tyr Ile Ile
 1 5 10 15
 Ile Phe Leu Thr Gly Leu Pro Ala Asn Leu Leu Ala Leu Arg Ala Phe
 20 25 30
 Val Gly Arg Ile Arg Gln Pro Gln Pro Ala Pro Val His Ile Leu Leu
 35 40 45
 Leu Ser Leu Thr Leu Ala Asp Leu Leu Leu Leu Leu Leu Leu Pro Phe
 50 55 60
 Lys Ile Ile Glu Ala Ala Ser Asn Phe Arg Trp Tyr Leu Pro Lys Val
 65 70 75 80
 Val Cys Ala Leu Thr Ser Phe Gly Phe Tyr Ser Ser Ile Tyr Cys Ser
 85 90 95
 Thr Trp Leu Leu Ala Gly Ile Ser Ile Glu Arg Tyr Leu Gly Val Ala
 100 105 110
 Phe Pro Val Gln Tyr Lys Leu Ser Arg Arg Pro Leu Tyr Gly Val Ile
 115 120 125
 Ala Ala Leu Val Ala Trp Val Met Ser Phe Gly His Cys Thr Ile Val
 130 135 140
 Ile Ile Val Gln Tyr Leu Asn Thr Thr Glu Gln Val Arg Ser Gly Asn
 145 150 155 160

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Glu Ile Thr Cys Tyr Glu Asn Phe Thr Asp Asn Gln Leu Asp Val Val
 165 170 175
 Leu Pro Val Arg Leu Glu Leu Cys Leu Val Leu Phe Phe Ile Pro Met
 180 185 190
 5 Ala Val Thr Ile Phe Cys Tyr Trp Arg Phe Val Trp Ile Met Leu Ser
 195 200 205
 Gln Pro Leu Val Gly Ala Gln Arg Arg Arg Arg Ala Lys Gly Leu Ala
 210 215 220
 10 Val Val Thr Leu Leu Asn Phe Leu Val Cys Phe Gly Pro Tyr Asn Val
 225 230 235 240
 Ser His Leu Val Gly Tyr His Gln Arg Lys Ser Pro Trp Trp Arg Ser
 245 250 255
 Ile Ala Val Val Phe Ser Ser Leu Asn Ala Ser Leu Asp Pro Leu Leu
 260 265 270
 15 Phe Tyr Phe Ser Ser Ser Val Val Arg Arg Ala Phe Gly Arg Gly Leu
 275 280 285
 Gln Val Leu Arg Asn Gln Gly Ser Ser Leu Leu Gly Arg Arg Gly Lys
 290 295 300
 20 Asp Thr Ala Glu Gly Thr Asn Glu Asp Arg Gly Val Gly Gln Gly Glu
 305 310 315 320
 Gly Met Pro Ser Ser Asp Phe Thr Thr Glu
 325 330

(278) INFORMATION FOR SEQ ID NO:277:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2724 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

ATGGACACCT CCCGGCTCGG TGTGCTCCTG TCCTTGCTG TGCTGCTGCA GCTGGCGACC 60
 GGGGGCAGCT CTCCCAGGTC TGGTGTGTTG CTGAGGGGCT GCCCCACACA CTGTCATTGC 120
 GAGCCCGACG GCAGGATGTT GCTCAGGGTG GACTGCTCCG ACCTGGGGCT CTCGGAGCTG 180
 CCTTCCAACC TCAGCGTCTT CACCTCTAC CTAGACCTCA GTATGAACAA CATCAGTCAG 240
 35 CTGCTCCCGA ATCCCCTGCC CAGTCTCCGC TTCCTGGAGG AGTTACGTCT TCGGGGAAAC 300

	GCTCTGACAT	ACATTCCCAA	GGGAGCATT	ACTGGCCTTT	ACAGTCTTAA	AGTTCTTATG	360
	CTGCAGAATA	ATCAGCTAAG	ACACGTACCC	ACAGAAGCTC	TGCAGAATTT	GCGAAGCCTT	420
	CAATCCCTGC	GTCTGGATGC	TAACCACATC	AGCTATGTGC	CCCCAAGCTG	TTTCAGTGGC	480
	CTGCATTCCC	TGAGGCACCT	GTGGCTGGAT	GACAAATGCGT	TAACAGAAAT	CCCCGTCCAG	540
5	GCTTTTAGAA	GTTTATCGGC	ATTGCAAGCC	ATGACCTTGG	CCCTGAACAA	AATACACCAC	600
	ATACCAGACT	ATGCCTTTGG	AAACCTCTCC	AGCTTGCTAG	TTCTACATCT	CCATAACAAT	660
	AGAATCCACT	CCCTGGGAAA	GAAATGCTTT	GATGGGCTCC	ACAGCCTAGA	GACTTTAGAT	720
	TTAAATTACA	ATAACCTTGA	TGAATTCCCC	ACTGCAATTA	GGACACTCTC	CAACCTTAAA	780
	GAAGTAGGAT	TTCATAGCAA	CAATATCAGG	TCGATACCTG	AGAAAGCATT	TGTAGGCAAC	840
10	CCTTCTCTTA	TTACAATACA	TTTCTATGAC	AATCCCATCC	AATTTGTTGG	GAGATCTGCT	900
	TTTCAACATT	TACCTGAACT	AAGAACACTG	ACTCTGAATG	GTGCCCTCACA	AATAACTGAA	960
	TTTCCTGATT	TAAGTGAAC	TGCAAACTG	GAGAGTCTGA	CTTTAACTGG	AGCACAGATC	1020
	TCATCTCTTC	CTCAAACCGT	CTGCAATCAG	TTACCTAATC	TCCAAGTGCT	AGATCTGTCT	1080
	TACAACCTAT	TAGAAGATTT	ACCCAGTTTT	TCAGTCTGCC	AAAAGCTTCA	GAAAATTGAC	1140
15	CTAAGACATA	ATGAAATCTA	CGAAATTAAA	GTTGACACTT	TCCAGCAGTT	GCTTAGCCTC	1200
	CGATCGCTGA	ATTTGGCTTG	GAACAAAATT	GCTATTATT	ACCCCAATGC	ATTTTCCACT	1260
	TTGCCATCCC	TAATAAGCT	GGACCTATCG	TCCAACCTCC	TGTCGTCTTT	TCCTATAACT	1320
	GGGTTACATG	GTTTAACTCA	CTTAAAATTA	ACAGGAAATC	ATGCCTTACA	GAGCTTGATA	1380
	TCATCTGAAA	ACTTTCCAGA	ACTCAAGGTT	ATAGAAATGC	CTTATGCTTA	CCAGTGCTGT	1440
20	GCATTTGGAG	TGTGTGAGAA	TGCCTATAAG	ATTTCTAATC	AATGGAATAA	AGGTGACAAC	1500
	AGCAGTATGG	ACGACCTTCA	TAAGAAAGAT	GCTGGAATGT	TTCAGGCTCA	AGATGAACGT	1560
	GACCTTGAAG	ATTTCTGCT	TGACTTTGAG	GAAGACCTGA	AAGCCCTTCA	TTCAGTGCAG	1620
	TGTTACACCT	CCCCAGGCC	CTTCAAACCC	TGTGAACACC	TGCTTGATGG	CTGGCTGATC	1680
	AGAATTGGAG	TGTGGACCAT	AGCAGTTCTG	GCACCTTACT	GTAATGCTTT	GGTGACTTCA	1740
25	ACAGTTTTCA	GATCCCCTCT	GTACATTTCC	CCCATTAAAC	TGTTAATTGG	GGTCATCGCA	1800
	GCAGTGAACA	TGCTCACGGG	AGTCTCCAGT	GCCGTGCTGG	CTGGTGTGGA	TGCGTTCACT	1860
	TTTGGCAGCT	TTGCACGACA	TGGTGCCTGG	TGGGAGAATG	GGGTTGGTTG	CCATGTCATT	1920
	GGTTTTTTGT	CCATTTTTGC	TTCAGAATCA	TCTGTTTTCC	TGCTTACTCT	GGCAGCCCTG	1980

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GAGCGTGGGT TCTCTGTGAA ATATTCTGCA AAATTTGAAA CGAAAGCTCC ATTTTCTAGC 2040
 CTGAAAGTAA TCATTTTGCT CTGTGCCCTG CTGGCCTTGA CCATGGCCGC AGTTCCCCTG 2100
 CTGGGTGGCA GCAAGTATGG CGCCTCCCCT CTCTGCCTGC CTTTGCCTTT TGGGGAGCCC 2160
 AGCACCATGG GCTACATGGT CGCTCTCATC TTGCTCAATT CCCTTTGCTT CCTCATGATG 2220
 5 ACCATTGCCT ACACCAAGCT CTA CTGCAAT TTGGACAAGG GAGACCTGGA GAATATTTGG 2280
 GACTGCTCTA TGAAAAACA CATTGCCCTG TTGCTCTTCA CCAACTGCAT CCTAAACTGC 2340
 CCTGTGGCTT TCTTGTCTT CTCTCTTTA ATAAACCTTA CATTATCAG TCCTGAAGTA 2400
 ATTAAGTTTA TCCTTCTGGT GGTAGTCCCA CTCTCTGCAT GTCTCAATCC CCTTCTCTAC 2460
 ATCTTGTTCA ATCCTCACTT TAAGGAGGAT CTGGTGAGCC TGAGAAAGCA AACCTACGTC 2520
 10 TGGACAAGAT CAAAACACCC AAGCTTGATG TCAATTA ACT CTGATGATGT CGAAAAACAG 2580
 TCCTGTGACT CAACTCAAGC CTGGTAACC TTTACCAGCT CCAGCATCAC TTATGACCTG 2640
 CCTCCAGTT CCGTGCCATC ACCAGCTTAT CCACTGACTG AGAGCTGCCA TCTTCTCTCT 2700
 GTGGCAATTG TCCCATGTCT CTAA 2724

(279) INFORMATION FOR SEQ ID NO:278:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 907 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant
- 20 (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:
- | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Thr | Ser | Arg | Leu | Gly | Val | Leu | Leu | Ser | Leu | Pro | Val | Leu | Leu |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Gln | Leu | Ala | Thr | Gly | Gly | Ser | Ser | Pro | Arg | Ser | Gly | Val | Leu | Leu | Arg |
| 25 | | | 20 | | | | | 25 | | | | | 30 | | |
| Gly | Cys | Pro | Thr | His | Cys | His | Cys | Glu | Pro | Asp | Gly | Arg | Met | Leu | Leu |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Arg | Val | Asp | Cys | Ser | Asp | Leu | Gly | Leu | Ser | Glu | Leu | Pro | Ser | Asn | Leu |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| 30 | Ser | Val | Phe | Thr | Ser | Tyr | Leu | Asp | Leu | Ser | Met | Asn | Asn | Ile | Ser |
| | 65 | | | | | 70 | | | | | 75 | | | | 80 |
| Leu | Leu | Pro | Asn | Pro | Leu | Pro | Ser | Leu | Arg | Phe | Leu | Glu | Glu | Leu | Arg |
| | | | 85 | | | | | 90 | | | | | | 95 | |

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Leu Ala Gly Asn Ala Leu Thr Tyr Ile Pro Lys Gly Ala Phe Thr Gly
 100 105 110

Leu Tyr Ser Leu Lys Val Leu Met Leu Gln Asn Asn Gln Leu Arg His
 115 120 125

5 Val Pro Thr Glu Ala Leu Gln Asn Leu Arg Ser Leu Gln Ser Leu Arg
 130 135 140

Leu Asp Ala Asn His Ile Ser Tyr Val Pro Pro Ser Cys Phe Ser Gly
 145 150 155 160

10 Leu His Ser Leu Arg His Leu Trp Leu Asp Asp Asn Ala Leu Thr Glu
 165 170 175

Ile Pro Val Gln Ala Phe Arg Ser Leu Ser Ala Leu Gln Ala Met Thr
 180 185 190

Leu Ala Leu Asn Lys Ile His His Ile Pro Asp Tyr Ala Phe Gly Asn
 195 200 205

15 Leu Ser Ser Leu Val Val Leu His Leu His Asn Asn Arg Ile His Ser
 210 215 220

Leu Gly Lys Lys Cys Phe Asp Gly Leu His Ser Leu Glu Thr Leu Asp
 225 230 235 240

20 Leu Asn Tyr Asn Asn Leu Asp Glu Phe Pro Thr Ala Ile Arg Thr Leu
 245 250 255

Ser Asn Leu Lys Glu Leu Gly Phe His Ser Asn Asn Ile Arg Ser Ile
 260 265 270

Pro Glu Lys Ala Phe Val Gly Asn Pro Ser Leu Ile Thr Ile His Phe
 275 280 285

25 Tyr Asp Asn Pro Ile Gln Phe Val Gly Arg Ser Ala Phe Gln His Leu
 290 295 300

Pro Glu Leu Arg Thr Leu Thr Leu Asn Gly Ala Ser Gln Ile Thr Glu
 305 310 315 320

30 Phe Pro Asp Leu Thr Gly Thr Ala Asn Leu Glu Ser Leu Thr Leu Thr
 325 330 335

Gly Ala Gln Ile Ser Ser Leu Pro Gln Thr Val Cys Asn Gln Leu Pro
 340 345 350

Asn Leu Gln Val Leu Asp Leu Ser Tyr Asn Leu Leu Glu Asp Leu Pro
 355 360 365

35 Ser Phe Ser Val Cys Gln Lys Leu Gln Lys Ile Asp Leu Arg His Asn
 370 375 380

Glu Ile Tyr Glu Ile Lys Val Asp Thr Phe Gln Gln Leu Leu Ser Leu

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	385		390		395		400									
	Arg	Ser	Leu	Asn	Leu	Ala	Trp	Asn	Lys	Ile	Ala	Ile	Ile	His	Pro	Asn
				405					410						415	
5	Ala	Phe	Ser	Thr	Leu	Pro	Ser	Leu	Ile	Lys	Leu	Asp	Leu	Ser	Ser	Asn
				420					425					430		
	Leu	Leu	Ser	Ser	Phe	Pro	Ile	Thr	Gly	Leu	His	Gly	Leu	Thr	His	Leu
			435					440					445			
	Lys	Leu	Thr	Gly	Asn	His	Ala	Leu	Gln	Ser	Leu	Ile	Ser	Ser	Glu	Asn
		450				455						460				
10	Phe	Pro	Glu	Leu	Lys	Val	Ile	Glu	Met	Pro	Tyr	Ala	Tyr	Gln	Cys	Cys
	465					470					475				480	
	Ala	Phe	Gly	Val	Cys	Glu	Asn	Ala	Tyr	Lys	Ile	Ser	Asn	Gln	Trp	Asn
				485						490					495	
15	Lys	Gly	Asp	Asn	Ser	Ser	Met	Asp	Asp	Leu	His	Lys	Lys	Asp	Ala	Gly
			500						505					510		
	Met	Phe	Gln	Ala	Gln	Asp	Glu	Arg	Asp	Leu	Glu	Asp	Phe	Leu	Leu	Asp
			515					520					525			
	Phe	Glu	Glu	Asp	Leu	Lys	Ala	Leu	His	Ser	Val	Gln	Cys	Ser	Pro	Ser
		530				535						540				
20	Pro	Gly	Pro	Phe	Lys	Pro	Cys	Glu	His	Leu	Leu	Asp	Gly	Trp	Leu	Ile
	545					550					555				560	
	Arg	Ile	Gly	Val	Trp	Thr	Ile	Ala	Val	Leu	Ala	Leu	Thr	Cys	Asn	Ala
				565						570					575	
25	Leu	Val	Thr	Ser	Thr	Val	Phe	Arg	Ser	Pro	Leu	Tyr	Ile	Ser	Pro	Ile
			580						585					590		
	Lys	Leu	Leu	Ile	Gly	Val	Ile	Ala	Ala	Val	Asn	Met	Leu	Thr	Gly	Val
		595					600						605			
	Ser	Ser	Ala	Val	Leu	Ala	Gly	Val	Asp	Ala	Phe	Thr	Phe	Gly	Ser	Phe
		610					615					620				
30	Ala	Arg	His	Gly	Ala	Trp	Trp	Glu	Asn	Gly	Val	Gly	Cys	His	Val	Ile
	625					630					635				640	
	Gly	Phe	Leu	Ser	Ile	Phe	Ala	Ser	Glu	Ser	Ser	Val	Phe	Leu	Leu	Thr
				645						650					655	
35	Leu	Ala	Ala	Leu	Glu	Arg	Gly	Phe	Ser	Val	Lys	Tyr	Ser	Ala	Lys	Phe
			660						665					670		
	Glu	Thr	Lys	Ala	Pro	Phe	Ser	Ser	Leu	Lys	Val	Ile	Ile	Leu	Leu	Cys
		675						680					685			

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Ala Leu Leu Ala Leu Thr Met Ala Ala Val Pro Leu Leu Gly Gly Ser
690 695 700

Lys Tyr Gly Ala Ser Pro Leu Cys Leu Pro Leu Pro Phe Gly Glu Pro
705 710 715 720

5 Ser Thr Met Gly Tyr Met Val Ala Leu Ile Leu Leu Asn Ser Leu Cys
725 730 735

Phe Leu Met Met Thr Ile Ala Tyr Thr Lys Leu Tyr Cys Asn Leu Asp
740 745 750

10 Lys Gly Asp Leu Glu Asn Ile Trp Asp Cys Ser Met Lys Lys His Ile
755 760 765

Ala Leu Leu Leu Phe Thr Asn Cys Ile Leu Asn Cys Pro Val Ala Phe
770 775 780

Leu Ser Phe Ser Ser Leu Ile Asn Leu Thr Phe Ile Ser Pro Glu Val
785 790 795 800

15 Ile Lys Phe Ile Leu Leu Val Val Val Pro Leu Pro Ala Cys Leu Asn
805 810 815

Pro Leu Leu Tyr Ile Leu Phe Asn Pro His Phe Lys Glu Asp Leu Val
820 825 830

20 Ser Leu Arg Lys Gln Thr Tyr Val Trp Thr Arg Ser Lys His Pro Ser
835 840 845

Leu Met Ser Ile Asn Ser Asp Asp Val Glu Lys Gln Ser Cys Asp Ser
850 855 860

Thr Gln Ala Leu Val Thr Phe Thr Ser Ser Ser Ile Thr Tyr Asp Leu
865 870 875 880

25 Pro Pro Ser Ser Val Pro Ser Pro Ala Tyr Pro Val Thr Glu Ser Cys
885 890 895

His Leu Ser Ser Val Ala Phe Val Pro Cys Leu
900 905

(280) INFORMATION FOR SEQ ID NO:279:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 35 (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

CATGCCAACC GGCCCGCGAG GCTGCTGCTG GT

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(281) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

ACCAGCAGCA GCCTCGCGGG CCGGTTGGCA TG

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INTERNATIONAL SEARCH REPORT

Int. Patent Application No
PCT/US 99/23938

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/12 C07K14/72 G01N33/50 G01N33/566

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 C12N C07K G01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	KJELSBERG M. A. ET AL.: "CONSTITUTIVE ACTIVATION OF THE ALPHA1B-ADRENERGIC RECEPTOR BY ALL AMINO ACID SUBSTITUTIONS AT A SINGLE SITE" JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 267, no. 3, 25 January 1992 (1992-01-25), pages 1430-1433, XP002911764 ISSN: 0021-9258 the whole document --- -/--	1,2, 4-13, 15-33, 35-37,41

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents:

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document but published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

- "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- "Z" document member of the same patent family

Date of the actual completion of the international search

2 March 2000

Date of mailing of the international search report

09/03/2000

Name and mailing address of the ISA

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Fax: (+31-70) 340-3016

Authorized officer

Mandl, B

INTERNATIONAL SEARCH REPORT

Int'l. Application No
PCT/US 99/23938

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	SCHEER A. ET AL.: "CONSTITUTIVELY ACTIVE G PROTEIN-COUPLED RECEPTORS: POTENTIAL MECHANISMS OF RECEPTOR ACTIVATION" JOURNAL OF RECEPTOR AND SIGNAL TRANSDUCTION RESEARCH, vol. 17, no. 1/03, 1997, pages 57-73, XP000867531 ISSN: 1079-9893 the whole document	1,2, 4-13, 15-33, 35-37,41
X	WO 97 21731 A (NEW ENGLAND MEDICAL CENTER INC) 19 June 1997 (1997-06-19) the whole document, especially Fig. 2-3	1,2,4, 9-13, 20-32, 35-37,41
X	WO 98 38217 A (HERRICK DAVIS KATHARINE ;TEITLER MILT (US); EGAN CHRISTINA C (US)) 3 September 1998 (1998-09-03) the whole document, especially page 7, lines 24-27, and figure 4	1,2, 4-13, 15-33, 35-37,41
P,X	PAUWELS P. J. ET AL.: "REVIEW: AMINO ACID DOMAINS INVOLVED IN CONSTITUTIVE ACTIVATION OF G-PROTEIN-COUPLED RECEPTORS" MOLECULAR NEUROBIOLOGY, vol. 17, no. 1/03, 1998, pages 109-135, XP000866477 ISSN: 0893-7648 the whole document	1,2, 4-13, 15-33, 35-37,41

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 99/ 23938

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☒ Claims Nos.: 34, 38-40, 42, 43
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
See FURTHER INFORMATION sheet PCT/ISA/210
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International Application No. PCT/US 99 23938

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box 1.2

Claims Nos.: 34,38-40,42,43

Claims 34, 38-40, 42 and 43 refer to compounds with an agonistic effect on a GPCR without giving a true technical characterization. Moreover, no such specific compounds are defined in the application. In consequence, the scope of said claims is ambiguous and vague, and their subject-matter is not sufficiently disclosed and supported (Art. 5 and 6 PCT). No search can be carried out for such purely speculative claims whose wording is, in fact, a mere recitation of the results to be achieved.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

INTERNATIONAL SEARCH REPORT

information on patent family members

International Application No

PCT/US 99/23938

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9721731 A	19-06-1997	US 5750353 A	12-05-1998
		AU 1334397 A	03-07-1997
		CA 2239293 A	19-06-1997
		EP 0869975 A	14-10-1998
WO 9838217 A	03-09-1998	AU 6343998 A	18-09-1998